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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 9.76923 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-15  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	3	US-08-783-853A-8
2	30	100.0	5	3	US-09-344-050-8
3	30	100.0	74	3	US-09-134-001C-3503
4	30	100.0	92	3	US-08-783-853A-84
5	30	100.0	92	3	US-09-344-050-84
6	30	100.0	112	3	US-08-783-853A-20
7	30	100.0	112	3	US-09-344-050-20
8	30	100.0	115	3	US-08-483-749A-24
9	30	100.0	117	1	US-08-249-013-6
10	30	100.0	117	2	US-08-886-863-6
11	30	100.0	117	3	US-09-175-229-6
12	30	100.0	117	5	PCT-US95-06764-6
13	30	100.0	118	1	US-08-425-336-124
14	30	100.0	118	1	US-08-425-336-126
15	30	100.0	118	1	US-08-488-113B-124
16	30	100.0	118	1	US-08-488-113B-126
17	30	100.0	118	1	US-08-477-484B-124
18	30	100.0	118	1	US-08-477-484B-126
19	30	100.0	118	1	US-08-107-669D-28
20	30	100.0	118	1	US-08-107-669D-29
21	30	100.0	118	1	US-08-107-669D-66
22	30	100.0	118	1	US-08-472-788A-28
23	30	100.0	118	1	US-08-472-788A-29
24	30	100.0	118	1	US-08-472-788A-88
25	30	100.0	118	1	US-08-472-788A-89
26	30	100.0	118	1	US-08-477-531B-28
27	30	100.0	118	2	US-08-477-531B-28

28	30	100.0	118	2	US-08-477-531B-29	Sequence 29, Appl
29	30	100.0	118	2	US-08-477-531B-66	Sequence 66, Appl
30	30	100.0	118	2	US-08-477-531B-67	Sequence 67, Appl
31	30	100.0	118	2	US-08-646-360-124	Sequence 124, App
32	30	100.0	118	2	US-08-646-360-126	Sequence 126, App
33	30	100.0	118	2	US-08-082-842A-28	Sequence 28, Appl
34	30	100.0	118	2	US-08-082-842A-29	Sequence 29, Appl
35	30	100.0	118	2	US-08-082-842A-88	Sequence 88, Appl
36	30	100.0	118	2	US-08-082-842A-89	Sequence 89, Appl
37	30	100.0	118	3	US-08-839-765-124	Sequence 124, App
38	30	100.0	118	3	US-09-136-389-124	Sequence 126, App
39	30	100.0	118	3	US-09-136-389-126	Sequence 124, App
40	30	100.0	118	3	US-09-610-838-124	Sequence 126, App
41	30	100.0	118	3	US-09-610-838-126	Sequence 96, Appl
42	30	100.0	118	4	US-09-440-781-96	Sequence 124, App
43	30	100.0	118	4	US-09-711-485-124	Sequence 126, App
44	30	100.0	118	4	US-09-711-485-126	
45	30	100.0	118	4	US-09-711-485-126	

ALIGNMENTS

RESULT 1  
US-08-783-853A-8  
; Sequence 8, Application US/08783853A  
; Patent No. 6005091  
; GENERAL INFORMATION:  
; APPLICANT: Blackburn, Michael  
; APPLICANT: Church, William  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Feuerstein, Giora  
; APPLICANT: Nichols, Andrew  
; APPLICANT: Padlan, Eduardo  
; APPLICANT: Patel, Arunbhai  
; APPLICANT: Sylvester, Daniel  
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/783, 853A  
; FILING DATE: 16-JAN-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029, 119  
; FILING DATE: 24-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumeister, Kirk  
; REGISTRATION NUMBER: 33, 833  
; REFERENCE/DOCKET NUMBER: P50438  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5096  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-08-783-853A-8

Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
11111  
Db 1 NYGMN 5

## RESULT 2

US-09-344-050-8  
Sequence 8, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-09-344-050-8

Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 NYGMN 5  
11111  
Db 1 NYGMN 5

## RESULT 3

US-09-134-001C-3503  
Sequence 3503, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3503  
LENGTH: 74  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3503

Query Match 100.0%; Score 30; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
11111  
Db 4 NYGMN 8

## RESULT 4

US-08-783-853A-84  
Sequence 84, Application US/08783853A  
Patent No. 6005091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-84

Query Match 100.0%; Score 30; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 8 NYGMN 12

## RESULT 5

US-09-344-050-84  
Sequence 84, Application US/09344050  
Patent No. 6391299

## GENERAL INFORMATION:

APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-84

Query Match 100.0%; Score 30; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 8 NYGMN 12

## RESULT 6

US-08-783-853A-20  
Sequence 20, Application US/08783853A  
Patent No. 6005091

## GENERAL INFORMATION:

APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:

TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-20

Query Match 100.0%; Score 30; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 28 NYGMN 32

## RESULT 7

US-09-344-050-20  
Sequence 20, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-20

Query Match 100.0%; Score 30; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 28 NYGMN 32

## RESULT 8

US-08-483-749A-24  
Sequence 24, Application US/08483749A  
Patent No. 6054561  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-749A-24

Query Match 100.0%; Score 30; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 31 NYGMN 35

## RESULT 9

US-08-249-013-6  
Sequence 6, Application US/08249013  
Patent No. 5643754  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,013  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: IutA  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-08-249-013-6

Query Match 100.0%; Score 30; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 22 NYGMN 26

RESULT 10  
US-08-886-863-6  
Sequence 6, Application US/08886863  
Patent No. 5824321  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/886,863  
FILING DATE: 01-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,013  
FILING DATE: 25-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: IutA  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-08-886-863-6

Query Match 100.0%; Score 30; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 22 NYGMN 26

RESULT 11  
US-09-175-229-6  
Sequence 6, Application US/09175229  
Patent No. 6309641  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/175,229  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,013  
FILING DATE: 25-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: IutA  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-09-175-229-6

Query Match 100.0%; Score 30; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

|||||  
Db 22 NYGMN 26

## RESULT 12

PCT-US95-06764-6

; Sequence 6, Application PC/TUS9506764

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: California

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/06764

; FILING DATE: 25-MAY-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Ph.D., Lisa A.,

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: PD3602

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 678-5070

; TELEFAX: (619) 678-5099

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; CLONE: lula

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..117

; PCT-US95-06764-6

Query Match 100.0%; Score 30; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||

Db 22 NYGMN 26

## RESULT 13

US-08-425-336-124

; Sequence 124, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; TITLE OF INVENTION: Proteins

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp; Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

COUNTRY: USA  
ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,336

; FILING DATE: 18-APR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.

; REGISTRATION NUMBER: P-36,989

; REFERENCE/DOCKET NUMBER: 31394

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 124:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 118 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-425-336-124

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
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Db 31 NYGMN 35

## RESULT 14

US-08-425-336-126

; Sequence 126, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; TITLE OF INVENTION: Proteins

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp; Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,336

; FILING DATE: 18-APR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-126

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 31 NYGMN 35

RESULT 15  
US-08-488-113B-124  
Sequence 124, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-9155  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-124

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 31 NYGMN 35

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 26.7692 Seconds  
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Title: US-10-071-962-15  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
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Searched: 1385339 seqs, 328044528 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	9	US-09-965-099-8 Sequence 8, Appli
2	30	100.0	5	10	US-09-791-551-74 Sequence 74, Appli
3	30	100.0	5	13	US-10-051-852-8 Sequence 8, Appli
4	30	100.0	5	14	US-10-071-962-15 Sequence 15, Appli
5	30	100.0	5	15	US-10-430-176-8 Sequence 8, Appli
6	30	100.0	5	15	US-10-377-121-26 Sequence 26, Appli
7	30	100.0	10	9	US-09-056-160B-1 Sequence 1, Appli
8	30	100.0	10	14	US-10-234-671-1 Sequence 1, Appli
9	30	100.0	10	16	US-10-018-245A-1 Sequence 1, Appli
10	30	100.0	10	16	US-10-723-434-111 Sequence 111, App
11	30	100.0	10	16	US-10-723-434-112 Sequence 112, App
12	30	100.0	10	16	US-10-723-434-116 Sequence 116, App
13	30	100.0	10	16	US-10-723-434-122 Sequence 122, App

14	30	100.0	12	10	US-09-954-385-147	Sequence 147, App
15	30	100.0	67	14	US-10-243-130-19	Sequence 19, Appli
16	30	100.0	70	14	US-10-243-130-17	Sequence 17, Appli
17	30	100.0	70	14	US-10-243-130-18	Sequence 18, Appli
18	30	100.0	76	15	US-10-424-599-268610	Sequence 268610,
19	30	100.0	92	9	US-09-965-099-84	Sequence 84, Appli
20	30	100.0	92	13	US-10-051-852-84	Sequence 84, Appli
21	30	100.0	92	15	US-10-430-176-84	Sequence 84, Appli
22	30	100.0	112	9	US-09-965-099-20	Sequence 20, Appli
23	30	100.0	112	13	US-10-051-852-20	Sequence 20, Appli
24	30	100.0	112	15	US-10-430-176-20	Sequence 20, Appli
25	30	100.0	116	9	US-09-971-543-8	Sequence 8, Appli
26	30	100.0	116	9	US-09-971-543-9	Sequence 9, Appli
27	30	100.0	116	9	US-09-971-543-10	Sequence 10, Appli
28	30	100.0	116	14	US-10-138-727A-2	Sequence 2, Appli
29	30	100.0	116	14	US-10-138-727A-4	Sequence 4, Appli
30	30	100.0	116	14	US-10-138-727A-6	Sequence 6, Appli
31	30	100.0	116	14	US-10-138-727A-17	Sequence 17, Appli
32	30	100.0	116	14	US-10-138-727A-18	Sequence 18, Appli
33	30	100.0	116	14	US-10-138-727A-19	Sequence 19, Appli
34	30	100.0	116	14	US-10-138-727A-20	Sequence 20, Appli
35	30	100.0	116	14	US-10-138-727A-21	Sequence 21, Appli
36	30	100.0	116	14	US-10-138-727A-22	Sequence 22, Appli
37	30	100.0	116	14	US-10-138-727A-23	Sequence 23, Appli
38	30	100.0	116	14	US-10-138-727A-24	Sequence 24, Appli
39	30	100.0	116	14	US-10-138-727A-25	Sequence 25, Appli
40	30	100.0	116	14	US-10-138-727A-26	Sequence 26, Appli
41	30	100.0	116	14	US-10-310-719-30	Sequence 30, Appli
42	30	100.0	116	14	US-10-310-719-33	Sequence 33, Appli
43	30	100.0	116	15	US-10-468-370-658	Sequence 658, App
44	30	100.0	116	15	US-10-468-370-660	Sequence 660, App
45	30	100.0	116	15	US-10-468-370-662	Sequence 662, App

ALIGNMENTS

RESULT 1  
US-09-965-099-8  
; Sequence 8, Application US/09965099  
; Patent No. US20020136725A1  
; GENERAL INFORMATION:  
; APPLICANT: Blackburn, Michael  
; Feuerstein, Gloria  
; Patel, Arunbhai  
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN  
; TREATMENT OF THROMBOSIS  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/965, 099  
; FILING DATE: 26-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/346,487  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumelster, Kirk  
; REGISTRATION NUMBER: 33,833  
; REFERENCE/DOCKET NUMBER: P50438-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5096



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; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 5 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: Internal
;   ORIGINAL SOURCE:
;     SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-965-099-8

Query Match      100.0%; Score 30; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYGMN 5
Db      1 NYGMN 5

RESULT 2
US-09-791-551-74
; Sequence 74, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
;   APPLICANT: KLOETZER, WILLIAM S.
;   APPLICANT: HANNA, NABIL
;   TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
;   FILE REFERENCE: 037003/0277869
;   CURRENT APPLICATION NUMBER: US/09/791,551
;   PRIOR FILING DATE: 2001-02-26
;   PRIOR APPLICATION NUMBER: 60/185,390
;   PRIOR FILING DATE: 2000-02-28
;   PRIOR APPLICATION NUMBER: 60/233,625
;   PRIOR FILING DATE: 2000-09-18
;   NUMBER OF SEQ ID NOS: 119
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 74
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-791-551-74

Query Match      100.0%; Score 30; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYGMN 5
Db      1 NYGMN 5

RESULT 3
US-10-051-852-8
; Sequence 8, Application US/10051852
; Publication No. US20020146411A1
; GENERAL INFORMATION:
;   APPLICANT: Blackburn, Michael
;   APPLICANT: Church, William
;   APPLICANT: Gross, Mitchell
;   APPLICANT: Feuerstein, Giora
;   APPLICANT: Nichols, Andrew
;   APPLICANT: Padiam, Eduardo
;   APPLICANT: Patel, Arunbhai
;   APPLICANT: Sylvester, Daniel
;   TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
;   OF THROMBOSIS
;   NUMBER OF SEQUENCES: 111
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```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/051,852
;   FILING DATE: 17-Jan-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/344,050
;     FILING DATE: 25-JUN-1999
;     APPLICATION NUMBER: 08/783,853
;     FILING DATE: 16-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Baumeister, Kirk
;     REGISTRATION NUMBER: 33,833
;     REFERENCE/DOCKET NUMBER: P50438
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 610-270-5096
;       TELEFAX: <Unknown>
;       TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: Internal
;     ORIGINAL SOURCE:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-051-852-8

Query Match      100.0%; Score 30; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYGMN 5
Db      1 NYGMN 5

RESULT 4
US-10-071-962-15
; Sequence 15, Application US/10071962
; Publication No. US20030170237A1
; GENERAL INFORMATION:
;   APPLICANT: Baifu Ni
;   APPLICANT: Bill N.C. Sun
;   APPLICANT: Cedilly R.Y. Sun
;   TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
;   Screening Method Therefor
;   FILE REFERENCE: 98-3
;   CURRENT APPLICATION NUMBER: US/10/071,962
;   CURRENT FILING DATE: 2002-02-08
;   PRIOR APPLICATION NUMBER: US/09/303,155A
;   PRIOR FILING DATE: 1999-04-30
;   PRIOR APPLICATION NUMBER: 60/083,575
;   PRIOR FILING DATE: 1998-04-30
;   NUMBER OF SEQ ID NOS: 27
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 15
;   LENGTH: 5
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; TYPE: PRT  
; ORGANISM: mouse  
US-10-071-962-15

Query Match 100.0%; Score 30; DB 14; length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
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Db 1 NYGMN 5

## RESULT 5

US-10-430-176-8  
; Sequence 8, Application US/10430176  
; Publication No. US20030235587A1  
; GENERAL INFORMATION:  
; APPLICANT: Feuerstein, Giora Z.  
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
; FILE REFERENCE: P50816-1  
; CURRENT APPLICATION NUMBER: US/10/430,176  
; PRIOR FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 09/817,960  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/359,202  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 60/095,714  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 10/051,852  
; PRIOR FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 09/344,050  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 08/783,853  
; PRIOR FILING DATE: 1997-01-06  
; PRIOR APPLICATION NUMBER: 60/010,018  
; PRIOR FILING DATE: 199-01-17  
; PRIOR APPLICATION NUMBER: 60/029,119  
; PRIOR FILING DATE: 1996-10-24  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Home sapiens  
US-10-430-176-8

Query Match 100.0%; Score 30; DB 15; length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
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Db 1 NYGMN 5

## RESULT 6

US-10-377-121-26  
; Sequence 26, Application US/10377121  
; Publication No. US20040001825A1  
; GENERAL INFORMATION:  
; APPLICANT: GOVINDAM, SERENGULAM  
; APPLICANT: OU, ZHENGXING  
; APPLICANT: HANSEN, HANS  
; APPLICANT: GOLDENBERG, DAVID  
; TITLE OF INVENTION: RS7 ANTIBODIES  
; FILE REFERENCE: 018733/1163  
; CURRENT APPLICATION NUMBER: US/10/377,121  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 60/360,299  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-377-121-26

Query Match 100.0%; Score 30; DB 15; length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 1 NYGMN 5

## RESULT 7

US-09-056-160B-1  
; Sequence 1, Application US/09056160B  
; Patent No. US20020032315A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,160B  
; FILING DATE: 06-Apr-1998  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/054,856  
; FILING DATE: 06-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1093R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-056-160B-1

Query Match 100.0%; Score 30; DB 9; length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 6 NYGMN 10

## RESULT 8

US-10-234-671-1  
; Sequence 1, Application US/10234671

Publication No. US20030190317A1  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/234,671  
FILING DATE: 03-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/056160  
FILING DATE: 06-APR-1998  
APPLICATION NUMBER: 60/126446  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: 60/054856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093R2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-234-671-1  
Query Match 100.0%; Score 30; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 6 NYGMN 10  
RESULT 9  
US-10-018-245A-1  
Sequence 1, Application US/10018245A  
Publication No. US20040115196A1  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, Yoshiaki  
APPLICANT: NAGAHIRA, Kazuhiro  
APPLICANT: NAKANISHI, Toshihiro  
TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complemer  
FILE REFERENCE: 46224  
CURRENT APPLICATION NUMBER: US/10/018,245A  
PRIOR FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: JP 117394/2000  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1  
LENGTH: 10  
TYPE: PRT  
ORGANISM: mouse  
FEATURE:  
OTHER INFORMATION: CDR-H1 of anti-human TNF-alpha antibody  
US-10-018-245A-1  
Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 6 NYGMN 10  
RESULT 10  
US-10-723-434-111  
Sequence 111, Application US/10723434  
Publication No. US20040133357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu  
APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Heieh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709.501  
CURRENT APPLICATION NUMBER: US/10/723,434  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 111  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDR1  
US-10-723-434-111  
Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 6 NYGMN 10  
RESULT 11  
US-10-723-434-112  
Sequence 112, Application US/10723434  
Publication No. US20040133357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu  
APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Heieh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709.501  
CURRENT APPLICATION NUMBER: US/10/723,434  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407

```
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/CDR1
US-10-723-434-112
```

```
Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10
```

```
RESULT 12
US-10-723-434-116
; Sequence 116, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 116
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/CDR1
US-10-723-434-116
```

```
Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10
```

```
RESULT 13
US-10-723-434-122
; Sequence 122, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
```

```
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/CDR1
US-10-723-434-122
```

```
Query Match      100.0%; Score 30; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10
```

```
RESULT 14
US-09-954-385-147
; Sequence 147, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-147
```

```
Query Match      100.0%; Score 30; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NYGMN 5
        |||||
Db      6 NYGMN 10
```

```
RESULT 15
US-10-243-130-19
```

; Sequence 19, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED  
; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-10-243-130-19

Query Match 100.0%; Score 30; DB 14; Length 67;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
|||  
Db 25 NYGMN 29

Search completed: March 1, 2005, 17:52:49  
Job time : 27.7692 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 6.76923 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-15  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	93	2	C24672	Ig heavy chain V r
2	30	100.0	99	2	S26326	Ig heavy chain V r
3	30	100.0	101	2	D24672	Ig heavy chain V r
4	30	100.0	105	2	S24764	Ig heavy chain V r
5	30	100.0	105	2	S24765	Ig heavy chain V r
6	30	100.0	109	2	S26325	Ig heavy chain V r
7	30	100.0	115	2	S19968	Ig heavy chain V r
8	30	100.0	115	2	S19965	Ig heavy chain V r
9	30	100.0	116	2	S69305	hypothetical prote
10	30	100.0	118	2	S19967	Ig heavy chain V r
11	30	100.0	119	2	A53285	Ig heavy chain V a
12	30	100.0	120	2	B42848	L6 mAb heavy chain
13	30	100.0	120	2	S12953	Ig heavy chain V r
14	30	100.0	124	2	PH1404	Ig heavy chain V r
15	30	100.0	146	4	S33905	Ig heavy chain pre
16	30	100.0	139	2	B90406	geranylgeranyl hyd
17	30	100.0	725	2	S01042	aerobactin recepto
18	30	100.0	726	2	AB0122	probable ferric si
19	30	100.0	732	2	T44483	receptor-like prot
20	27	90.0	96	2	B90793	hypothetical prote
21	27	90.0	96	2	G85653	hypothetical prote
22	27	90.0	151	2	E70615	hypothetical prote
23	27	90.0	153	2	G75616	nodulation protein
24	27	90.0	174	2	F85028	hypothetical prote
25	27	90.0	191	2	A97074	hypothetical prote
26	27	90.0	212	2	D84442	probable glutathio
27	27	90.0	281	2	S34496	hypothetical prote
28	27	90.0	321	2	D97836	tetraacyldisacchar
29	27	90.0	326	1	VGXR37	glycoprotein VP7 p

30	27	90.0	326	1	VGXR7H	glycoprotein VP7 p
31	27	90.0	326	1	VGXRMD	glycoprotein VP7 p
32	27	90.0	326	1	VGXRWA	glycoprotein VP7 p
33	27	90.0	329	2	T13016	hypothetical prote
34	27	90.0	338	2	T28779	hypothetical prote
35	27	90.0	340	2	T28080	hypothetical prote
36	27	90.0	344	2	H45252	pilV constant regi
37	27	90.0	373	2	A69143	galactosyl-transfe
38	27	90.0	381	2	T40341	hypothetical prote
39	27	90.0	388	2	A82903	conserved hypothet
40	27	90.0	391	2	E83840	hypothetical prote
41	27	90.0	406	2	JC4600	isocitrate dehydro
42	27	90.0	454	2	A97147	siderophore/Surfac
43	27	90.0	470	1	S14628	phosphogluconate d
44	27	90.0	560	2	S09995	nuclear factor I-B
45	27	90.0	561	2	A31256	transcription fact

ALIGNMENTS

RESULT 1  
C24672  
Ig heavy chain V region (VMU-1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999  
C;Accession: C24672  
R;Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985  
A;Reference number: A91022; MUID:86055722; PMID:2998759  
A;Accession: C24672  
A;Molecule type: DNA  
A;Residues: 1-93 <WIN>  
A;Cross-references: GB:X03300; NID:G52375; PIDN:CAA27039.1; PID:G773221  
A;Note: this sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 100.0%; Score 30; DB 2; Length 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 12 NYGMN 16

RESULT 2  
S26326  
Ig heavy chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 17-Apr-1998  
C;Accession: S26326  
R;Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A;Reference number: S26309; MUID:91341421; PMID:1908510  
A;Accession: S26326  
A;Molecule type: mRNA  
A;Residues: 1-99 <STA>  
A;Cross-references: EMBL:X59174  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 100.0%; Score 30; DB 2; Length 99;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 11 NYGMN 15

## RESULT 3

D24672

Ig heavy chain V region (VGAM3-8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999

C:Accession: D24672

R:Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A:Reference number: A91022; MUID:86055722; PMID:2998759

A:Accession: D24672

A:Molecule type: DNA

A:Residues: 1-101 &lt;WIN&gt;

A:Cross-references: GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:g773215

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 101;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5  
|||||

DB 12 NYGMN 16

## RESULT 4

S24764

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C:Accession: S24764; S24772; S24777

R:Klages, S.

submitted to the EMBL Data Library, August 1992

A:Reference number: S24763

A:Accession: S24764

A:Molecule type: DNA

A:Residues: 1-105 &lt;KLA&gt;

A:Cross-references: EMBL:Z14999

A:Accession: S24772

A:Molecule type: DNA

A:Residues: 1-105 &lt;KLW&gt;

A:Cross-references: EMBL:Z15011

R:Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A:Reference number: S24776

A:Accession: S24777

A:Molecule type: DNA

A:Residues: 1-105 &lt;THO&gt;

A:Cross-references: EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID:g52617

C:Genetics: 9/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 105;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5  
|||||

DB 43 NYGMN 47

## RESULT 5

S24765

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C:Accession: S24765; S24773; S24778

R:Klages, S.

submitted to the EMBL Data Library, August 1992

A:Reference number: S24763

A:Accession: S24765

A:Molecule type: DNA

A:Residues: 1-105 &lt;KLA&gt;

A:Cross-references: EMBL:Z15001

A:Accession: S24773

A:Molecule type: DNA

A:Residues: 1-105 &lt;KLW&gt;

A:Cross-references: EMBL:Z15013

R:Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A:Reference number: S24776

A:Accession: S24778

A:Molecule type: DNA

A:Residues: 1-105 &lt;THO&gt;

A:Cross-references: EMBL:Z15022; NID:g52619; PIDN:CAA78741.1; PID:g52620

C:Genetics: 9/1

A:Introns: 9/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 105;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5  
|||||

DB 43 NYGMN 47

## RESULT 6

S26325

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S26325

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein ei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26325

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 &lt;STA&gt;

A:Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:g52080; PID:g1334043

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F.5-88/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 109;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NYGMN 5  
|||||

DB 21 NYGMN 25

## RESULT 7

S19968

Ig heavy chain V region (M-T408) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S19968

R:Weissenhorn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19968

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-115 &lt;WEI&gt;

A:Cross-references: UNIPROT:Q921A6; EMBL:X65089

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 26 NYGMN 30

RESULT 8

S19965  
Ig heavy chain V region (M-T321) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S19965  
R;Weissenhorn, W.; Riethmuelier, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19965  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-115 <WEI>

A;Cross-references: UNIPROT:Q921A6; EMBL:X65088  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 24 NYGMN 28

RESULT 9

S69305

hypothetical protein YLR280C - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein L8003.10-b  
C;Species: Saccharomyces cerevisiae  
C;Date: 20-Jul-1996 #sequence\_revision 23-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: S69305  
R;Pauley, A.  
submitted to the EMBL Data Library, November 1994  
A;Description: The sequence of S. cerevisiae cosmid 8003.  
A;Reference number: S50366  
A;Accession: S69305  
A;Molecule type: DNA  
A;Residues: 1-116 <PAU>

A;Cross-references: UNIPROT:O13541; EMBL:U17243; NID:g596030; PIDN:AAB67350.1; PID:g2340  
C;Genetics:  
A;Gene: MIPS:YLR280C  
A;Cross-references: SGD:S0004270  
A;Map position: 12R  
C;Superfamily: Saccharomyces hypothetical protein YLR280C

Query Match 100.0%; Score 30; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 19 NYGMN 23

RESULT 10

S19967

Ig heavy chain V region (M-T406) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S19967  
R;Weissenhorn, W.; Riethmuelier, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19967  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-118 <WEI>

A;Cross-references: UNIPROT:Q921A6; EMBL:X65090  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 28 NYGMN 32

RESULT 11

A53285

Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C;Accession: A53285  
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
Mol. Immunol. 28, 1063-1072, 1991  
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struc  
and their pH-reactivity profiles.  
A;Reference number: A53285; MUID:92017897; PMID:1922102  
A;Accession: A53285  
A;Status: preliminary  
A;Molecule type: DNA; protein  
A;Residues: 1-119 <SAW>

A;Cross-references: GB:D12736; NID:g220595; PIDN:BAA02228.1; PID:g220596  
A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:P:63299)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
Db 31 NYGMN 35

RESULT 12

B42848

L6 mAb heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B42848; S33903  
R;Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo  
J. Biol. Chem. 267, 15552-15558, 1992  
A;Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and characte  
A;Reference number: A42848; WUID:92348410; PMID:1639794  
A;Accession: B42848  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-120 <FEI>

A;Cross-references: GB:M90690; NID:g195065; PIDN:AAA38146.1; PID:g195066  
A;Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBI:P:109961)  
A;Accession: S33903  
A;Status: preliminary





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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 32.3846 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-15  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	30	100.0	116	2 O13541	O13541 saccharomyc
2	30	100.0	175	1 H1S5 BUCDN	Q84156 buchnera ap
3	30	100.0	226	2 Q73DT4	Q73dt4 bacillus ce
4	30	100.0	244	2 Q65151	Q65151 bacillus li
5	30	100.0	261	2 Q6WDM4	Q6wdk4 acomy's igni
6	30	100.0	299	2 Q924G6	Q924g6 meriones sh
7	30	100.0	300	2 Q6WDM3	Q6wdm3 beamys hind
8	30	100.0	301	2 Q6WDM2	Q6wdm2 cricetomys
9	30	100.0	302	2 Q924G5	Q924g5 gerbillurus
10	30	100.0	305	2 Q895E8	Q895e8 clostridium
11	30	100.0	316	2 Q9CLC4	Q9clc4 pasteurella
12	30	100.0	323	2 Q8XS16	Q8xs16 ralsconia s
13	30	100.0	326	2 Q39726	Q39726 human rotav
14	30	100.0	326	2 Q85033	Q85033 porcine rot
15	30	100.0	326	2 Q9E3T9	Q9e3t9 human rotav
16	30	100.0	332	2 Q814Y5	Q814y5 plasmodium
17	30	100.0	341	2 Q9N2S8	Q9n2s8 caenorhabdi
18	30	100.0	342	2 Q8XN57	Q8xn57 clostridium
19	30	100.0	387	2 Q65HS8	Q65hs8 bacillus li
20	30	100.0	398	2 Q97WB3	Q97wb3 sulfolobus
21	30	100.0	422	2 Q7URZ8	Q7urz8 rhodospirell
22	30	100.0	423	2 Q975B4	Q975b4 sulfolobus
23	30	100.0	479	2 Q7SBB0	Q7sbb0 neurospora
24	30	100.0	725	2 Q6J3R6	Q6j3r6 escherichia
25	30	100.0	726	2 Q66619	Q66619 yersinia ps
26	30	100.0	726	2 Q8ZHB0	Q8znb0 yersinia pe
27	30	100.0	729	2 Q8KR53	Q8kr53 escherichia
28	30	100.0	731	2 Q7UB05	Q7ub05 shigella fl
29	30	100.0	731	2 Q6DBU6	Q6dbu6 erwinia car
30	30	100.0	732	1 IUTR ECOLI	P14542 escherichia
31	30	100.0	732	2 Q93PE2	Q93pe2 shigella bo

32	30	100.0	732	2 Q6Q7N8	Q6q7n8 escherichia
33	30	100.0	732	2 Q9XCH0	Q9xch0 shigella fl
34	30	100.0	733	2 Q6KD44	Q6kd44 escherichia
35	30	100.0	733	2 Q6U607	Q6u607 klebsiella
36	30	100.0	759	2 Q83PM3	Q83pm3 shigella fl
37	30	100.0	759	2 Q8FDM0	Q8fdw0 escherichia
38	30	100.0	828	2 Q8SX93	Q8sx93 drosophila
39	30	100.0	828	2 Q9VBX0	Q9vbx0 drosophila
40	30	100.0	1119	2 Q815N6	Q815n6 plasmodium
41	30	100.0	1133	2 Q6CMR8	Q6cmr8 kluyveromyc
42	30	100.0	1480	2 Q7RN37	Q7rn37 plasmodium
43	30	100.0	1959	2 Q8V3G5	Q8v3g5 swinepox vi
44	27	90.0	36	2 Q809B8	Q809b8 human rotav
45	27	90.0	36	2 Q809C3	Q809c3 human rotav

ALIGNMENTS

RESULT 1

O13541 PRELIMINARY; PRT; 116 AA.

AC O13541; MEDLINE=97313267; PubMed=9169871;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE Y1r280CP.  
GN Name=YLR280C;  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=97313267; PubMed=9169871;  
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,  
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,  
RA Entlian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,  
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,  
RA Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,  
RA Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,  
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,  
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,  
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,  
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,  
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";  
RL Nature 387:0-0(0).  
RN [2]

RP SEQUENCE FROM N.A.  
RA Pauley A.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [4]

RP SEQUENCE FROM N.A.  
RA Cherry J.M.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U17243; AAB67350.1; -.  
DR PIR; S69305; S69305.  
SQ SEQUENCE 116 AA; 12951 MW; E31414157730E032 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 NYGMN 5  
Db 19 NYGMN 23



```
RESULT 2
HIS5_BUCDN STANDARD; PRT; 175 AA.
ID HIS5_BUCDN
AC Q84I56;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH) (Fragment).
GN Name=hisH;
OS Buchnera aphidicola (subsp. Diuraphis noxia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118101;
RN [1]
RP SEQUENCE FROM N.A.
RA Moran N.A., Mira A.;
RT "Levels of selection on genes of mutualistic endosymbionts.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate. The hisH subunit provides the ammonia necessary to amidotransferase activity that produces the ammonia necessary to hisF for the synthesis of IGP and AICAR (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
-----
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-----
CC EMBL; AF465524; AAC33042.1; -.
DR HAMAP; MF_00278; -.
DR InterPro; IPR000991; GATase_1.
DR InterPro; IPR010139; IMP_synth_hisH.
DR Pfam; PF00117; GATase; 1.
DR TIGRFAMs; TIGR01855; IMP_synth_hisH; 1.
DR PROSITE; PS00442; GATASE_TYPE_I; 1.
KW Glutamine amidotransferase; Histidine biosynthesis; Transferase.
FT ACT_SITE 78 78 By similarity.
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 19540 MW; E50851BA299D89C3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 1; Length 175;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 159 NYGMN 163

RESULT 3
Q73DT4 PRELIMINARY; PRT; 226 AA.
AC Q73DT4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE0627;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
```

```
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017266; AAS39561.1; -.
DR TIGR; BCE0627; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 226 AA; 25834 MW; 9CCB16555AD97185 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 226;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 218 NYGMN 222

RESULT 4
Q65L51 PRELIMINARY; PRT; 244 AA.
AC Q65L51;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein (Peptidoglycan-binding LysM, peptidoglycan-binding LysM).
GN ORFNames=BL01953, BLi01309;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Gelleron N., Ehrlich S.D., Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU40213.1; -.
DR EMBL; CP000002; AAU22864.1; -.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 25925 MW; 1561DF77670470E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 244;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
Db 42 NYGMN 46

RESULT 5
```

Q6WDM4  
ID Q6WDM4 PRELIMINARY; PRT; 261 AA.  
AC Q6WDM4;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN Name=GHR;  
OS Acomys ignitus (fiery spiny mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Acomys.  
OX NCBI\_TaxID=60745;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stepan S.J., Adkins R.M., Anderson J.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY294923; AAQ62681.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 261 261  
SQ SEQUENCE 261 AA; 28136 MW; FF3641198C9807A3 CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 261;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 185 NYGMN 189

RESULT 6  
Q924G6  
ID Q924G6 PRELIMINARY; PRT; 299 AA.  
AC Q924G6;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN Name=GHR;  
OS Meriones shawi (Shaw's jird).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Meriones.  
OX NCBI\_TaxID=37435;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21219190; PubMed=11319262;  
RA Adkins R.M., Gelke E.L., Rowe D., Honeycutt R.L.;  
RT "Molecular phylogeny and divergence time estimates for major rodent  
RT groups: evidence from multiple genes."  
RL Mol. Biol. Evol. 18:777-791(2001).  
DR EMBL; AF332021; AAK71897.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 299 299  
SQ SEQUENCE 299 AA; 32452 MW; 5E624460D1D7243E CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 299;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 198 NYGMN 202

RESULT 7  
Q6WDM3  
ID Q6WDM3 PRELIMINARY; PRT; 300 AA.  
AC Q6WDM3;

DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN Name=GHR;  
OS Beamys hindel (long-tailed pouched rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;  
OC Beamys.  
OX NCBI\_TaxID=70596;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stepan S.J., Adkins R.M., Anderson J.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY294904; AAQ62662.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 300 300  
SQ SEQUENCE 300 AA; 32730 MW; 5211AC3F179BA984 CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 199 NYGMN 203

RESULT 8  
Q6WDM2  
ID Q6WDM2 PRELIMINARY; PRT; 301 AA.  
AC Q6WDM2;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN Name=GHR;  
OS Cricetomys gambianus (Gambia rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;  
OC Cricetomys.  
OX NCBI\_TaxID=10085;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stepan S.J., Adkins R.M., Anderson J.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY294905; AAQ62663.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 301 301  
SQ SEQUENCE 301 AA; 32706 MW; F599E104ECAF57D CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 301;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 200 NYGMN 204

RESULT 9  
Q924G5  
ID Q924G5 PRELIMINARY; PRT; 302 AA.  
AC Q924G5;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN Name=GHR;

OS Gerbillurus vailianus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Gerbillurus.  
OX NCBI\_TaxID=49440;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21219190; PubMed=11319262;  
RA Adkins R.M., Gelke E.L., Rowe D., Honeycutt R.L.;  
RT "Molecular phylogeny and divergence time estimates for major rodent  
RT groups: evidence from multiple genes."  
RL Mol. Biol. Evol. 18:777-791(2001).  
DR EMBL; AF332022; AAK71898.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
KM Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 302 302  
SQ SEQUENCE 302 AA; 32687 MW; C08D7478B24CEAC3 CRC64;  
  
Query Match 100.0%; Score 30; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 201 NYGMN 205

## RESULT 10

Q895E8 PRELIMINARY; PRT; 305 AA.  
AC Q895E8;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein CTC01328.  
GN OrderedLocusNames=CTC01328;  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Massachusetts / E88;  
RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;  
RA Brueggemann H., Baumeier S., Fricke W.F., Wiewer A., Liesegang H.,  
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
RA Gottschalk G.;  
RT "The genome sequence of Clostridium tetani, the causative agent of  
RT tetanus disease."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
DR EMBL; AE015940; AAC035892.1; -  
KM Complete proteome.  
SQ SEQUENCE 305 AA; 34802 MW; 6AEC3E38786B98D8 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 24 NYGMN 28

## RESULT 11

Q9CLC4 PRELIMINARY; PRT; 316 AA.  
AC Q9CLC4;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE CorA.  
GN Name=CorA; OrderedLocusNames=PM1315;

OS Pasteurella multocida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Pasteurella.  
OX NCBI\_TaxID=747;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Pm70;  
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;  
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;  
RT "Complete genomic sequence of Pasteurella multocida Pm70."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
DR EMBL; AE006170; AAK03399.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0015087; F:cobalt ion transporter activity; IEA.  
DR GO; GO:0015095; F:magnesium ion transporter activity; IEA.  
DR GO; GO:0006824; P:cobalt ion transport; IEA.  
DR GO; GO:0015693; P:magnesium ion transport; IEA.  
DR InterPro; IPR004488; CorA\_transp.  
DR InterPro; IPR002523; Mg2+\_transpCOrA.  
DR Pfam; PF01544; CorA; 1.  
DR TIGRFAMs; TIGR00383; CorA; 1.  
KM Complete proteome.  
SQ SEQUENCE 316 AA; 36422 MW; AD3EF4C4BC0ACC99 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 275 NYGMN 279

## RESULT 12

Q8XS16 PRELIMINARY; PRT; 323 AA.  
AC Q8XS16;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE PROBABLE MAGNESIUM AND COBALT TRANSPORT TRANSMEMBRANE PROTEIN.  
GN Name=RS01784; OrderedLocusNames=RS0665;  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Plasmid megaplasmid.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GMT1000;  
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
RA Siguiet P., Thebault P., Whalen M., Wincker P., Levy M.,  
RA Weissenbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."  
RL Nature 415:497-502(2002).  
DR EMBL; AL646080; CAD17816.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0046873; F:metal ion transporter activity; IEA.  
DR GO; GO:0030001; P:metal ion transport; IEA.  
DR Pfam; PF01544; CorA; 1.  
KM Complete proteome.  
SQ SEQUENCE 323 AA; 36251 MW; DE264559E199DD61 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||

Db 282 NYGMN 286

## RESULT 13

039726 PRELIMINARY; PRT; 326 AA.  
ID 039726  
AC 039726;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE VP7.  
OS Human rotavirus G3.  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus A.  
OX NCBI\_TaxID=73036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97412814; PubMed=9267457;  
RA Wen L., Nakayama M., Yamanishi Y., Nishio O., Fang Z.-Y., Nakagomi O., Araki K., Nishimura S., Hasegawa A., Muller W.E., Ushijima H.;  
RT "Genetic variation in the VP7 gene of human rotavirus serotype 3 (G3 type) isolated in China and Japan."  
RL Arch. Virol. 142:1481-1489(1997).  
DR EMBL; D86274; BAA23294.1;  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
SQ SEQUENCE 326 AA; 37318 MW; ED2375A2CBA14234 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 326;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 52 NYGMN 56

## RESULT 14

085033 PRELIMINARY; PRT; 326 AA.  
ID 085033  
AC 085033;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Outer capsid protein VP7.  
OS Porcine rotavirus.  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ciarlet M., Luder J.E., Liprandi F.;  
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L35057; AAA47091.1;  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
SQ SEQUENCE 326 AA; 37078 MW; 36A21B861A8F8B3E CRC64;

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 326;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 52 NYGMN 56

## RESULT 15

09E3T9 PRELIMINARY; PRT; 326 AA.  
ID 09E3T9  
AC 09E3T9;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Outer capsid protein VP7.

OS Human rotavirus A.

OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.

OX NCBI\_TaxID=10941;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=97/S48;

RA Xu S., Wang J., Hung T.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF260957; AAG15360.1; -

DR GO; GO:0019028; C:viral capsid; IEA.

DR InterPro; IPR001963; VP7.

DR Pfam; PF00434; VP7; 1.

DR ProDom; PD000191; VP7; 1.

SQ SEQUENCE 326 AA; 37285 MW; 19479E95DAD21507 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 326;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

Db 52 NYGMN 56

Search completed: March 1, 2005, 17:43:10  
Job time : 34.3846 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 127.108 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-16  
Perfect score: 101  
Sequence: 1 WINTYTGPTYAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	101	100.0	17	3	AAy32224	Aay32224 G-CSF ago
2	95	94.1	117	8	AD126496	Adi26496 Human ECL
3	94	93.1	17	5	AAg80312	Aag80312 Anti-huma
4	94	93.1	17	8	ADs87337	Ads87337 Humanised
5	94	93.1	19	2	AAy17490	Aay17490 Mab 31.1
6	94	93.1	19	2	AAy08699	Aay08699 Human col
7	94	93.1	19	3	AAy83642	Aay83642 Biotin la
8	94	93.1	67	7	ADh62639	Adh62639 Mouse ant
9	94	93.1	70	7	ADh62638	Adh62638 Mouse ant
10	94	93.1	112	7	ADC27441	Adc27441 TMERF2#18
11	94	93.1	112	7	ADC27449	Adc27449 TMERF2#21
12	94	93.1	115	4	AAb84740	Aab84740 Variable
13	94	93.1	116	4	AAb84739	Aab84739 Variable
14	94	93.1	116	5	AAE37830	Aae27830 Mouse KS
15	94	93.1	116	5	AAE37839	Aae27839 Mouse KS
16	94	93.1	116	5	AAE37837	Aae27837 Mouse KS
17	94	93.1	116	5	AAE37825	Aae27825 Mouse KS
18	94	93.1	116	5	AAE37826	Aae27826 Mouse KS
19	94	93.1	116	5	AAE37828	Aae27828 Mouse KS
20	94	93.1	116	5	AAE37832	Aae27832 Mouse KS
21	94	93.1	116	5	AAE37834	Aae27834 Mouse KS
22	94	93.1	116	5	ADg67541	Adg67541 KS antibo
23	94	93.1	116	5	ADg67537	Adg67537 KS antibo
24	94	93.1	116	5	ADg67543	Adg67543 KS antibo
25	94	93.1	116	5	ADg67531	Adg67531 KS antibo

26	94	93.1	116	5	ADg67533	Adg67533 KS antibo
27	94	93.1	116	5	ADg67539	Adg67539 KS antibo
28	94	93.1	116	5	ADg67529	Adg67529 KS antibo
29	94	93.1	116	5	ADg67535	Adg67535 KS antibo
30	94	93.1	116	6	AAE33431	Aae33431 Murine KS
31	94	93.1	116	6	AAE33433	Aae33433 Murine KS
32	94	93.1	116	6	AAE33434	Aae33434 Murine KS
33	94	93.1	116	6	AAE33435	Aae33435 Murine KS
34	94	93.1	116	6	AAE33414	Aae33414 Murine KS
35	94	93.1	116	6	AAE33432	Aae33432 Murine KS
36	94	93.1	116	6	AAE33438	Aae33438 Murine KS
37	94	93.1	116	6	AAE33430	Aae33430 Murine KS
38	94	93.1	116	6	AAE33437	Aae33437 Murine KS
39	94	93.1	116	6	AAE33436	Aae33436 Murine KS
40	94	93.1	116	6	AAO30908	Aao30908 hu-KS ant
41	94	93.1	116	6	AAO30911	Aao30911 di-KS ant
42	94	93.1	117	2	AAr28752	Aar28752 Heavy cha
43	94	93.1	117	5	AAg80317	Aag80317 Anti-huma
44	94	93.1	117	5	AAE33439	Aae33439 Murine KS
45	94	93.1	118	2	AAr25414	Aar25414 Heavy cha

ALIGNMENTS

RESULT 1	AAy32224	standard; peptide; 17 AA.
AC	AAy32224;	
DT	15-FEB-2000	(first entry)
DE	G-CSF agonist antibody mAb163-93 heavy chain variable region CDR2.	
KW	Granulocyte colony stimulating factor receptor; G-CSF; mouse; monoclonal antibody; agonist; screening; neutropenia; therapy;	
KW	complementarity determining region; CDR; mAb163-93.	
OS	Mus musculus.	
PN	W09955735-A1.	
PD	04-NOV-1999.	
PF	30-APR-1999;	99WO-US009466.
PR	30-APR-1998;	98US-0083575P.
PA	(TANO-) TANOX INC.	
PI	Ni B, Sun BNC, Sun CRY,	
DR	WPI; 2000-052805/04.	
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic cell lineage progenitors.	
PS	Claim 13; Page 30; 64pp; English.	
CC	The present sequence represents complementarity determining region 2 (CDR2) of the heavy chain variable region of murine monoclonal antibody mAb163-93. This antibody is an example of an agonist molecule that specifically binds to or interacts with human granulocyte colony stimulating factor (G-CSF) receptor to stimulate cell proliferation and differentiation, especially by dimerising the receptor or activating phosphorylation of kinases associated with the receptor. Agonist antibodies can be used to stimulate leading to a repopulation of G-CSF-dependent cells, e.g. to differentiate leading to a repopulation of neutrophilic granulocyte lineage cells, especially to treat neutropenia (claimed). They can also be used to detect human G-CSF receptor immunologically	
CC	Sequence 17 AA;	

Query Match 100.0%; Score 101; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
| | | | | | | | | | | | | | | | |  
Db 1 WINTYTGPTYAGDFKG 17

RESULT 2  
AD126496  
ID AD126496 standard; protein; 117 AA.  
XX  
AC AD126496;  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Human ECL2B-3-H SEQ ID NO:32.  
XX

KW antibody; enzyme; virucide; anti-HIV; cytostatic; antibacterial;  
KW helicobacter pylori urease inhibitor;  
KW chemokine receptor CCR-5 antagonist; cancer; infectious disease;  
KW Helicobacter pylori; HIV; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004009805-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 18-JUL-2003; 2003WO-JP009147.  
XX

PR 19-JUL-2002; 2002JP-00211756.  
PR 19-JUL-2002; 2002JP-00211768.  
PR 27-FEB-2003; 2003JP-00051943.  
PR 17-JUL-2003; 2003JP-00198270.  
PR 17-JUL-2003; 2003JP-00198281.  
PR 17-JUL-2003; 2003JP-00198292.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Uda T, Hifumi E;  
XX  
DR WPI; 2004-132963/13.  
DR N-PSDB; AD126497.  
XX  
XX

PT Screening potential antibody enzymes by identification of a catalytic  
PT triplet residue in the stereostructure for production of antibody enzymes  
PT as diagnostic and therapeutic agents for cancer and infectious diseases  
PT including HIV infection.  
XX  
PS Disclosure; SEQ ID NO 32; 232pp; Japanese.  
XX  
XX

CC The invention relates to a novel method for producing antibody enzymes  
CC comprising a structural analysis step which confirms the existence in the  
CC predicted stereostructure of the antibody based on its amino acid  
CC sequence of a catalytic triplet residue structure in which a serine  
CC residue, an aspartic acid residue, and a histidine or glutamic acid  
CC residue are located sterically close to one another. An enzyme produced  
CC by the method of the invention has virucide, anti-HIV, cytostatic, and  
CC antibacterial activity. The enzyme acts as a helicobacter pylori urease  
CC inhibitor, or chemokine receptor CCR-5 (HIV target) antagonist. The  
CC method of the invention is useful for the treatment, prevention and  
CC diagnosis of cancer and infectious diseases, especially infection by  
CC Helicobacter pylori or HIV. The present sequence is used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 117 AA;

Query Match 94.1%; Score 95; DB 8; Length 117;  
Best Local Similarity 94.1%; Pred. No. 3e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
| | | | | | | | | | | | | | | | |  
Db 50 WINTYTGPTYAGDFMG 66

RESULT 3  
AAG80312  
ID AAG80312 standard; peptide; 17 AA.  
XX  
AC AAG80312;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Anti-human TNF-alpha CDR-H2 peptide.  
XX

KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;  
KW heavy chain; light chain; complementarity determining region; vasotropic;  
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;  
KW rheumatoid arthritis; malaria; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200179298-A1.  
XX  
PD 25-OCT-2001.  
XX  
PF 18-APR-2001; 2001WO-JP003308.  
XX  
PR 19-APR-2000; 2000JP-00117394.  
XX  
PA (SUNR ) SUNTORY LTD.  
XX  
PI Fukuda Y, Negahira K, Nakanishi T;  
XX  
DR WPI; 2002-066345/09.  
XX

PT Novel heavy and light-chain polypeptides of chimeric and humanized  
PT antibodies against human tumor necrosis factor alpha for low-  
PT immunogenicity treatment of TNF-related diseases such as toxic shock  
PT syndrome.  
XX  
XX  
PS Claim 1b; Page 25; 36pp; Japanese.  
XX  
XX

CC This invention describes novel heavy chain and light chain polypeptides  
CC or their fragments of a recombinant antibody to human TNF-alpha which  
CC contain complementarity determining region (CDR) sequences. The products  
CC of the invention have vasotropic, antiarthritic, neuroprotective and  
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in  
CC vivo. The antibodies are used for producing chimeric and humanised  
CC antibodies that may be used for the treatment and prevention of TNF-alpha  
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,  
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in  
CC humans. This sequence represents the anti-human tumour necrosis factor-  
CC alpha (TNF-alpha) heavy chain CDR1 designated CDR-H2  
XX  
SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 5; Length 17;  
Best Local Similarity 94.1%; Pred. No. 5.8e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
| | | | | | | | | | | | | | | | |  
Db 1 WINTYTGPTYADDFKG 17

RESULT 4  
ADS87337  
ID ADS87337 standard; peptide; 17 AA.  
XX  
AC ADS87337;  
XX

DT 18-NOV-2004 (first entry)  
XX  
DE Humanised antibody MN3 heavy chain variable region CDR2.  
XX  
KW cytosstatic; vasotropic; antimicrobial; antiinflammatory; antipyretic;  
KW antiatherosclerotic; cardiant; monoclonal antibody; NCA90; NCA95;  
KW chimeric antibody; humanized antibody; inflammation; appendicitis;  
KW inflammatory bowel disease; pelvic inflammatory disease; fever;  
KW cystic fibrosis; granulocyte related disorder; atherosclerosis;  
KW infarction; cancer; ischemic lesion; complementarity determining region.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
PN WO2004029093-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 30-SEP-2003; 2003WO-GB004229.  
XX  
PR 30-SEP-2002; 2002US-0414341P.  
XX  
PA (IMMU-) IMMUNOMEDICS INC.  
PA (MCCA/) MCCALL J D.  
XX  
PI Goldenberg DM, Hansen H, Leung S;  
XX  
DR WPI; 2004-329873/30.  
XX  
PT Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens,  
PT useful for treating malignancy, inflammation, atherosclerosis,  
PT infarction, or other granulocyte related disorders.  
XX  
PS Claim 4; Page 105; 134pp; English.  
XX  
XX The invention relates to a monoclonal antibody (Mab) (I) or its fragment  
CC that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90  
CC the Mab or its fragment is chimeric, partially humanized or fully  
CC humanized and where when the Mab or its fragment binds NCA95 the Mab or  
CC its fragment is either fully humanized or chimeric, partially humanized  
CC or fully humanized BW 250/183. (I) is useful for treating, detecting or  
CC imaging sites of inflammation resulting from appendicitis, inflammatory  
CC bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and  
CC treating granulocyte related disorders, atherosclerosis and infarction.  
CC (I) is useful for detecting or treating cancer or ischemic lesion. This  
CC sequence corresponds to the complementarity determining region 2 (CDR2)  
CC of the heavy chain of the antibody of the invention.  
XX  
SQ Sequence 17 AA;  
  
Query Match 93.1%; Score 94; DB 8; Length 17;  
Best Local Similarity 94.1%; Pred. No. 5.8e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WINTYTGPTYAGDFKG 17  
|||  
Db 1 WINTYTGPTYADDFKG 17  
|||  
  
RESULT 5  
AAY17490  
ID AAY17490 standard; peptide; 19 AA.  
XX  
AC AAY17490;  
XX  
DT 03-AUG-1999 (first entry)  
XX  
DE Mab 31.1 CDR sequence derived peptide COL311 H2.  
XX  
KW Heavy chain variable region; 2CAVHCOL1; light chain variable region;  
KW light chain consensus region; heavy chain consensus region; antibody;  
KW anti-idiotypic response; modified immunoglobulin; infectious disease;

KW cancer; vaccine.  
XX  
OS Synthetic.  
XX  
PN WO9925379-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 13-NOV-1998; 98WO-US024303.  
XX  
PR 14-NOV-1997; 97US-0065716P.  
PR 10-APR-1998; 98US-0081403P.  
XX  
PA (EURO-) EUROCELLTQUE SA.  
XX  
PI Burch RM;  
XX  
DR WPI; 1999-337877/28.  
XX  
PT Vaccines for generating an anti-idiotypic response to an antigen.  
XX  
PS Example; Page 55; 107pp; English.  
XX  
XX The present invention describes vaccines for generating an anti-idiotypic  
CC response to an antigen. Vaccine (A), comprises, apart from a carrier, a  
CC first immunoglobulin (I), comprising a variable region (V), or its  
CC fragment that includes V, which is identical to a second immunoglobulin  
CC (II), or its corresponding fragment, which can bind specifically to an  
CC antigen (Ag), except for one or more amino acid (aa) substitutions in V.  
CC These substitutions involve replacement of Cys residues involved in  
CC disulfide bridge formation by residues that do not contain a thiol group.  
CC (A) are used to raise an anti-idiotypic response (preferably both cellular  
CC and humoral), particularly for treating a wide range of tumours (or  
CC precancerous conditions) and infectious diseases (viral, bacterial, or  
CC fungal, parasitic), specifically syphilis, gonorrhea, acquired immune  
CC deficiency syndrome, malaria, Shigella, Salmonella, hepatitis A or C,  
CC Lyme disease, encephalitis, herpes, Gram-positive or -negative bacterial  
CC infections, or pneumococcal infections. Antibodies raised against the  
CC vaccine may be recovered and administered to a second subject. (I) may  
CC also be used for treating autoimmune diseases and allergy. Modifying (II)  
CC so that it can no longer form intrachain disulfide bridges reduces  
CC conformational constraints and results in significantly better anti-  
CC idiotypic responses. The present sequence represents a Mab 31.1 CDR  
CC sequence derived peptide from an example from the present invention  
XX  
SQ Sequence 19 AA;  
  
Query Match 93.1%; Score 94; DB 2; Length 19;  
Best Local Similarity 94.1%; Pred. No. 6.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WINTYTGPTYAGDFKG 17  
|||  
Db 3 WINTYTGPTYADDFKG 19  
|||  
  
RESULT 6  
AAY08699  
ID AAY08699 standard; protein; 19 AA.  
XX  
AC AAY08699;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human colon carcinoma-associated protein antigen binding fragment 5.  
XX  
KW Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;  
KW complementarity determining region; infectious disease agent antigen;  
KW cellular receptor; infectious agent; chemotherapeutic agent; vaccine;  
KW cancer; infectious disease; autoimmune disease; rheumatoid arthritis;  
KW ulcerative colitis; psoriasis; allergy; immunoassay reagent; diagnosis;  
KW veterinary medicine; antibody; immunisation; antibody; immune tolerance;  
KW human colon cancer-associated protein antigen; cryptic expression;

KW anti-idiotypic immune response.  
XX  
OS Homo sapiens.  
XX  
PN WO9925378-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 13-NOV-1998; 98WO-US024302.  
XX  
PR 14-NOV-1997; 97US-0065716P.  
PR 10-APR-1998; 98US-0081403P.  
XX  
PA (EURO-) EUROCELTIQUE SA.  
XX  
PI Burch RM;  
XX  
DR WPI; 1999-357555/30.  
XX  
PT Modified immunoglobulins including engineered binding site.  
XX  
PS Claim 6; Page 75; 123pp; English.  
XX  
CC This invention describes a novel modified immunoglobulin (mIg), or its  
CC fragment, that binds immunospecifically to one member (M1) of a binding  
CC pair comprising a variable domain (V) having at least one CDR  
CC (complementarity determining region) that contains a portion of the  
CC second member (M2) of the pair. This portion is not present in the  
CC natural CDR and M1 is a cancer antigen, infectious disease agent antigen,  
CC a cellular receptor for an infectious agent (provided the binding site is  
CC not NAMP or NVPD) or a member of a receptor-ligand pair. mIg (also  
CC related molecules containing the same V region), optionally coupled to a  
CC chemotherapeutic agent, are used in therapeutic and/or prophylactic  
CC compositions, or vaccines, against cancers, infectious or autoimmune  
CC diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or  
CC allergies. They can also be used as immunoassay reagents for diagnosing  
CC these conditions. mIg can be used in human or veterinary medicine. mIg  
CC have higher affinity or specificity than native antibodies. Manipulation  
CC of CDR ensures binding specificity and avoids the unpredictable  
CC immunization and screening procedures currently used. It is now possible  
CC to generate antibodies against antigens that are inaccessible, by virtue  
CC of immune tolerance or cryptic expression. mIg neutralize antigens  
CC directly or they induce an anti-idiotypic immune response. This sequence  
CC represents a fragment of modified immunoglobulin that immunospecifically  
CC binds to a binding pair in which the first member is the human colon  
CC carcinoma-associated protein antigen  
XX  
SQ Sequence 19 AA;  
  
Query Match 93.1%; Score 94; DB 2; Length 19;  
Best Local Similarity 94.1%; Pred. No. 6.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 3 WINTYTGEPYADDFKG 19  
  
RESULT 7  
ID AAY83642 standard; peptide; 19 AA.  
XX AAY83642;  
AC  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Biotin labelled peptide derived from CDR region of Mab31.1.  
XX  
KW Vaccine; contraceptive; antibody; monoclonal antibody; Mab;  
KW disulphide bond; complementary determining region; CDR; reproduction;  
KW immune response; anti-idiotypic response; light chain; heavy chain;  
KW variable region; SP-10 epitope.  
XX

OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= Biotinylated  
FT  
XX  
PN WO200029443-A1.  
XX  
PD 25-MAY-2000.  
XX  
PF 12-NOV-1999; 99WO-US026671.  
XX  
PR 13-NOV-1998; 98US-0108325P.  
XX  
PA (EURO-) EUROCELTIQUE SA.  
XX  
PI Burch RM, Sackler DA;  
XX  
DR WPI; 2000-387748/33.  
XX  
PT Novel vaccine composition useful as contraceptive comprises first  
PT immunoglobulin capable of inducing an anti-idiotypic response and  
PT identical to second immunoglobulin having complementarity determining  
PT region.  
XX  
PS Example 6.6, Page 40; 77pp; English.  
XX  
CC A new contraceptive vaccine is described which comprises an antibody  
CC which has at least one complementary determining region (CDR) containing  
CC a peptide fragment of a protein associated with reproductive function  
CC capable of eliciting an anti-idiotypic response. The antibody is modified  
CC such that one or more variable region cysteine residues that form  
CC intrachain disulfide bonds are substituted for amino acids lacking a  
CC sulphydryl group and incapable of forming such bonds e.g Alanine. The  
CC vaccine formulation is suitable for both males and females. The method is  
CC convenient, effective, does not pose health risks and is cheap. In a  
CC particular example, a modified antibody derived from the monoclonal  
CC antibody Mab31.1 which recognises an antigen on human colon carcinomas  
CC had alanine residues substituted for the cysteine residues at positions  
CC 22 and 92 of the heavy chain variable region and at positions 23 and 88  
CC of the light chain variable region. The modified variable regions were  
CC designated 2CAVHC0L1 and 2CAVLC0L1. Mab31.1, modified Mab31.1 and  
CC biotinylated peptides derived from the CDR's of Mab31.1 were injected  
CC into mice (See AAY83638-Y83643) in order to generate antisera against the  
CC CDR regions of Mab31.1 and the antibodies. This peptide was designated  
CC COL311H2  
XX  
SQ Sequence 19 AA;  
  
Query Match 93.1%; Score 94; DB 3; Length 19;  
Best Local Similarity 94.1%; Pred. No. 6.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 3 WINTYTGEPYADDFKG 19  
  
RESULT 8  
ID ADH62639 standard; protein; 67 AA.  
XX ADH62639;  
AC  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Mouse anti-IgE antibody heavy chain consensus.  
XX  
KW Mouse; IgE; antibody; heavy chain; primer; monoclonal antibody; HB134;  
KW H36.  
XX  
OS Synthetic.  
OS Mus sp.



XX PN US2003143682-A1.  
XX 31-JUL-2003.  
XX 13-SEP-2002; 2002US-00243130.  
XX PF 07-NOV-2000; 2000US-00707468.  
XX PR  
XX PA (NICO/) NICOLAIDES N C.  
XX PA (GRAS/) GRASSO L.  
XX PA (SASS/) SASS P M.  
XX PI Nicolaides NC, Grasso L, Sass PM;  
XX DR WPI; 2003-635957/60.  
XX PT Increasing affinity of a monoclonal antibody for an antigen by  
PT substituting amino acids within the antibody, useful for producing  
PT altered antibodies with enhanced biochemical activity.  
XX PS Example 6; SEQ ID NO 19; 30pp; English.  
XX CC The invention relates to increasing affinity of a monoclonal antibody for  
CC an antigen comprising substituting an amino acid within the variable  
CC domain of the heavy or light chain of the monoclonal antibody with a  
CC second amino acid having a non-polar side chain or with a proline where  
CC the amino acid comprises a non-polar side chain, and where the monoclonal  
CC antibody for the antigen is increased. Also disclosed are nucleic acids,  
CC polypeptides, vectors, host cells and transgenic animals used in the  
CC method of the invention. The methods and compositions of the present  
CC invention are useful for generating antibody-producing cells with  
CC increased level of antibody production. Cellular analysis of HB134 clones  
CC with higher Mab levels within the conditioned medium (CM) were analysed  
CC to determine if the increased production was simply due to genetic  
CC alterations at the Ig locus that may lead to over-expression of the  
CC polypeptides forming the antibody or due to enhanced secretion due to a  
CC genetic alteration affecting secretory pathway mechanisms. Three HB134  
CC clones that had increased levels of antibody within their CM were  
CC expanded. 10000 cells were prepared for western blot analysis to assay  
CC for intracellular steady state Ig protein levels. H36 cells were used as  
CC standard reference and a rodent fibroblast was used as an Ig negative  
CC control. Cells were pelleted by centrifugation and lysed directly in 300  
CC microl of SDS lysis buffer and boiled for 5 minutes. Lysate proteins were  
CC separated by electrophoresis on 4-12% NuPAGE gels for analysis of Ig  
CC heavy chain. Gels were electroblotted onto Immobilon-P in 48 mM Tris  
CC base, 40 mM glycine, 0.0375% SDS, 20% methanol and blocked at room  
CC temperature for 1 hour in Tris-buffered saline plus 0.05% Tween-20 and 5%  
CC condensed milk. The results showed an increased Ab production while  
CC others had a similar steady state level as the control sample, yet had  
CC higher levels of Ab within the CM. These data suggest a mechanism whereby  
CC a subset of HB134 clones contained a genetic alteration that in turn  
CC produces elevated secretion of antibody. HB134 was derived from H36 (an  
CC anti-human IGE antibody) by introducing a dominant negative mutant form  
CC of PMS2 (a deletion mutant lacking amino acids 134 onwards), a mismatch  
CC repair protein. The present sequence is a consensus heavy chain variable  
CC region from H36 and its mutant.  
XX SQ Sequence 67 AA;  
Query Match 93.1%; Score 94; DB 7; Length 67;  
Best Local Similarity 94.1%; Pred. No. 2.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AC ADH62638;  
XX 25-MAR-2004 (first entry)  
XX DT  
XX DE Mouse anti-IGE antibody H36 heavy chain.  
XX DE  
XX KW Mouse; IGE; antibody; Heavy chain; primer; monoclonal antibody; HB134;  
XX KW H36.  
XX OS Mus sp.  
XX OS  
XX PN US2003143682-A1.  
XX PD 31-JUL-2003.  
XX PF 13-SEP-2002; 2002US-00243130.  
XX PR 07-NOV-2000; 2000US-00707468.  
XX PA (NICO/) NICOLAIDES N C.  
XX PA (GRAS/) GRASSO L.  
XX PA (SASS/) SASS P M.  
XX PI Nicolaides NC, Grasso L, Sass PM;  
XX DR WPI; 2003-635957/60.  
XX PT Increasing affinity of a monoclonal antibody for an antigen by  
PT substituting amino acids within the antibody, useful for producing  
PT altered antibodies with enhanced biochemical activity.  
XX PS Claim 7; SEQ ID NO 18; 30pp; English.  
XX CC The invention relates to increasing affinity of a monoclonal antibody for  
CC an antigen comprising substituting an amino acid within the variable  
CC domain of the heavy or light chain of the monoclonal antibody with a  
CC second amino acid having a non-polar side chain or with a proline where  
CC the amino acid comprises a non-polar side chain, and where the monoclonal  
CC antibody for the antigen is increased. Also disclosed are nucleic acids,  
CC polypeptides, vectors, host cells and transgenic animals used in the  
CC method of the invention. The methods and compositions of the present  
CC invention are useful for generating antibody-producing cells with  
CC increased level of antibody production. Cellular analysis of HB134 clones  
CC with higher Mab levels within the conditioned medium (CM) were analysed  
CC to determine if the increased production was simply due to genetic  
CC alterations at the Ig locus that may lead to over-expression of the  
CC polypeptides forming the antibody or due to enhanced secretion due to a  
CC genetic alteration affecting secretory pathway mechanisms. Three HB134  
CC clones that had increased levels of antibody within their CM were  
CC expanded. 10000 cells were prepared for western blot analysis to assay  
CC for intracellular steady state Ig protein levels. H36 cells were used as  
CC standard reference and a rodent fibroblast was used as an Ig negative  
CC control. Cells were pelleted by centrifugation and lysed directly in 300  
CC microl of SDS lysis buffer and boiled for 5 minutes. Lysate proteins were  
CC separated by electrophoresis on 4-12% NuPAGE gels for analysis of Ig  
CC heavy chain. Gels were electroblotted onto Immobilon-P in 48 mM Tris  
CC base, 40 mM glycine, 0.0375% SDS, 20% methanol and blocked at room  
CC temperature for 1 hour in Tris-buffered saline plus 0.05% Tween-20 and 5%  
CC condensed milk. The results showed an increased Ab production while  
CC others had a similar steady state level as the control sample, yet had  
CC higher levels of Ab within the CM. These data suggest a mechanism whereby  
CC a subset of HB134 clones contained a genetic alteration that in turn  
CC produces elevated secretion of antibody. HB134 was derived from H36 (an  
CC anti-human IGE antibody) by introducing a dominant negative mutant form  
CC of PMS2 (a deletion mutant lacking amino acids 134 onwards), a mismatch  
CC repair protein. The present sequence is the wild-type heavy chain  
XX SQ Sequence 70 AA;  
Query Match 93.1%; Score 94; DB 7; Length 70;  
Best Local Similarity 94.1%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;





KW Heavy chain; antibody 3A2D3; polyglutamine expansion;  
KW neurodegenerative disorder; Huntington's disease.  
XX  
OS Mus musculus.  
XX  
PN WO200151522-A1.  
XX  
PD 19-JUL-2001.  
XX  
PF 05-JAN-2001; 2001WO-US000361.  
XX  
PR 07-JAN-2000; 2000US-00478960.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Finkbeiner S;  
XX  
DR WPI; 2001-451842/48.  
XX  
PT Novel antibody useful for detecting the presence of polyglutamine  
PT expansion comprising protein in a sample, binds to the protein in a  
PT manner that differs from the 1C2 monoclonal antibody.  
XX  
PS Disclosure; Page 18; 35pp; English.  
XX  
CC The present chain represents the variable region of the heavy chain of  
CC murine antibody 3A2D3. This antibody recognizes a protein having a  
CC polyglutamine expansion, where the number percentage of non-glutamine  
CC residues in the polyglutamine expansion does not exceed 10. The antibody  
CC binds to the protein in a manner that differs from the 1C2 monoclonal  
CC antibody. The antibodies are used to modulate intracellular binding  
CC activity of polyglutamine expansion. The antibodies are useful for  
CC detecting an agent capable of modulating the binding interaction between  
CC polyglutamine expansion comprising protein in a cell and a target of the  
CC protein. They are also useful in immunoassays that are capable of  
CC providing the detection of disease associated polyglutamine expansion  
CC containing proteins. The antibodies are useful for treating a host  
CC suffering from a disease condition associated with the presence of  
CC polyglutamine expansion containing protein, such as neurodegenerative  
CC disorders, e.g. Huntington's disease  
XX  
SQ Sequence 115 AA;  
  
Query Match 93.1%; Score 94; DB 4; Length 115;  
Best Local Similarity 94.1%; Pred. No. 4.1e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WINTYTGPTYAGDFKG 17  
|||  
Db 49 WINTYTGPTYADDFKG 65  
  
RESULT 13  
AAB84739  
ID AAB84739 standard; protein; 116 AA.  
XX  
AC AAB84739;  
XX  
DT 17-SEP-2001 (first entry)  
XX  
DE Variable region of the heavy chain of murine antibody IF1IE5.  
XX  
KW Heavy chain; antibody IF1IE5; polyglutamine expansion;  
KW neurodegenerative disorder; Huntington's disease.  
XX  
OS Mus musculus.  
XX  
PN WO200151522-A1.  
XX  
PD 19-JUL-2001.  
XX  
PF 05-JAN-2001; 2001WO-US000361.  
XX

PR 07-JAN-2000; 2000US-00478960.  
XX  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Finkbeiner S;  
XX  
DR WPI; 2001-451842/48.  
XX  
PT Novel antibody useful for detecting the presence of polyglutamine  
PT expansion comprising protein in a sample, binds to the protein in a  
PT manner that differs from the 1C2 monoclonal antibody.  
XX  
PS Disclosure; Page 18; 35pp; English.  
XX  
CC The present chain represents the variable region of the heavy chain of  
CC murine antibody IF1IE5. This antibody recognizes a protein having a  
CC polyglutamine expansion, where the number percentage of non-glutamine  
CC residues in the polyglutamine expansion does not exceed 10. The antibody  
CC binds to the protein in a manner that differs from the 1C2 monoclonal  
CC antibody. The antibodies are used to modulate intracellular binding  
CC activity of polyglutamine expansion. The antibodies are useful for  
CC detecting an agent capable of modulating the binding interaction between  
CC polyglutamine expansion comprising protein in a cell and a target of the  
CC protein. They are also useful in immunoassays that are capable of  
CC providing the detection of disease associated polyglutamine expansion  
CC containing proteins. The antibodies are useful for treating a host  
CC suffering from a disease condition associated with the presence of  
CC polyglutamine expansion containing protein, such as neurodegenerative  
CC disorders, e.g. Huntington's disease  
XX  
SQ Sequence 116 AA;  
  
Query Match 93.1%; Score 94; DB 4; Length 116;  
Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WINTYTGPTYAGDFKG 17  
|||  
Db 49 WINTYTGPTYADDFKG 65  
  
RESULT 14  
AAE27830  
ID AAE27830 standard; protein; 116 AA.  
XX  
AC AAE27830;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Mouse KS de-immunised VH2 modified epitope.  
XX  
KW Mouse; fusion protein; immunological; major histocompatibility complex;  
KW MHC; gastric upset; nausea; epitope; KS antibody.  
XX  
OS Mus sp.  
XX  
PN WO200266514-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 18-FEB-2002; 2002WO-EP001690.  
XX  
PR 19-FEB-2001; 2001EP-00103955.  
PR 05-APR-2001; 2001EP-00108291.  
XX  
PA (MERE ) MERCK PATENT GMBH.  
XX  
PI Gillies S, Carr FU, Jones T, Carter G, Hamilton A, Williams S;  
PI Hanlon M, Watkins J, Baker M, Way JC;  
XX  
DR WPI; 2002-667054/71.  
XX  
PT New modified fusion protein with reduced immunogenicity, useful for

PT combining favorable properties of a composition, comprises an  
PT immunoglobulin molecule linked to a non-immunoglobulin target  
PT polypeptide.  
XX  
PS Example 19; Page 75; 92pp; English.  
XX  
CC The invention relates to an immunogenically modified fusion protein  
CC derived from a parent fusion protein, comprising first and second  
CC proteins/polypeptides, where the first protein is an immunoglobulin  
CC molecule or its fragment and the second protein is non-immunoglobulin  
CC target polypeptide each linked to the other directly or by a linker  
CC molecule. The immunogenically modified fusion protein is useful in  
CC combining known favourable properties of a composition or in creating new  
CC properties of a composition which elicits biological or pharmacological  
CC efficacy without having undesirable physiological effects such as nausea  
CC or gastric upset. The present sequence is mouse KS antibody modified  
CC epitope. This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 116 AA;

Query Match 93.1%; Score 94; DB 5; Length 116;  
Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYTGPTYAGDFKG 17  
| | | | | | | | | | | | | | | | | |  
DB 50 WINTYTGPTYADDFKG 66

RESULT 15

AAE27839 ID AAE27839 standard; protein; 116 AA.

AC AAE27839;

DT 13-DEC-2002 (first entry)

DE Mouse KS VH protein #2.

XX Mouse; fusion protein; immunological; major histocompatibility complex;

KW MHC; gastric upset; nausea; KS antibody.

OS Mus sp.

PN WO200266514-A2.

PD 29-AUG-2002.

PF 18-FEB-2002; 2002WO-EP001690.

PR 19-FEB-2001; 2001EP-00103955.

PR 05-APR-2001; 2001EP-00108291.

PA (MERE ) MERCK PATENT GMBH.

PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;

PI Hanlon M, Watkins J, Baker M, Way JC;

DR WPI; 2002-667054/71.

PT New modified fusion protein with reduced immunogenicity, useful for  
PT combining favorable properties of a composition, comprises an  
PT immunoglobulin molecule linked to a non-immunoglobulin target  
PT polypeptide.

PS Example 19; Page 76; 92pp; English.

CC The invention relates to an immunogenically modified fusion protein  
CC derived from a parent fusion protein, comprising first and second  
CC proteins/polypeptides, where the first protein is an immunoglobulin  
CC molecule or its fragment and the second protein is non-immunoglobulin  
CC target polypeptide each linked to the other directly or by a linker  
CC molecule. The immunogenically modified fusion protein is useful in

CC combining known favourable properties of a composition or in creating new  
CC properties of a composition which elicits biological or pharmacological  
CC efficacy without having undesirable physiological effects such as nausea  
CC or gastric upset. The present sequence is mouse KS antibody protein. This  
CC sequence is used in the exemplification of the invention  
XX  
SQ Sequence 116 AA;

Query Match 93.1%; Score 94; DB 5; Length 116;  
Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYTGPTYAGDFKG 17  
| | | | | | | | | | | | | | | | | |  
DB 50 WINTYTGPTYADDFKG 66

Search completed: March 1, 2005, 17:36:03  
Job time : 128.108 secs

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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 33.2154 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-16  
Perfect score: 101  
Sequence: 1 WINTYTGPTYAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfil1est1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	90.1	160	4 US-09-318-786-35	Sequence 35, Appli
2	91	90.1	252	3 US-08-279-772A-6	Sequence 6, Appli
3	91	90.1	252	3 US-08-902-486-9	Sequence 9, Appli
4	89	88.1	118	1 US-08-425-336-124	Sequence 124, App
5	89	88.1	118	1 US-08-488-113B-124	Sequence 124, App
6	89	88.1	118	1 US-08-477-484B-124	Sequence 124, App
7	89	88.1	118	1 US-08-107-669D-28	Sequence 28, Appl
8	89	88.1	118	1 US-08-107-669D-29	Sequence 29, Appl
9	89	88.1	118	1 US-08-107-669D-66	Sequence 66, Appl
10	89	88.1	118	1 US-08-472-788A-28	Sequence 28, Appl
11	89	88.1	118	1 US-08-472-788A-29	Sequence 29, Appl
12	89	88.1	118	1 US-08-472-788A-88	Sequence 88, Appl
13	89	88.1	118	2 US-08-477-531B-28	Sequence 28, Appl
14	89	88.1	118	2 US-08-477-531B-29	Sequence 29, Appl
15	89	88.1	118	2 US-08-477-531B-66	Sequence 66, Appl
16	89	88.1	118	2 US-08-646-360-124	Sequence 124, App
17	89	88.1	118	2 US-08-082-842A-28	Sequence 28, Appl
18	89	88.1	118	2 US-08-082-842A-29	Sequence 29, Appl
19	89	88.1	118	2 US-08-082-842A-88	Sequence 88, Appl
20	89	88.1	118	3 US-08-839-765-124	Sequence 124, App
21	89	88.1	118	3 US-09-136-389-124	Sequence 124, App
22	89	88.1	118	3 US-09-610-838-124	Sequence 124, App
23	89	88.1	118	4 US-09-440-781-96	Sequence 96, Appl
24	89	88.1	118	4 US-09-440-781-97	Sequence 97, Appl
25	89	88.1	118	4 US-09-711-485-124	Sequence 124, App
26	89	88.1	121	4 US-09-440-781-98	Sequence 98, Appl
27	89	88.1	121	4 US-09-440-781-99	Sequence 99, Appl

28	89	88.1	491	4 US-10-011-125A-2	Sequence 2, Appli
29	86	85.1	140	3 US-08-569-147-76	Sequence 76, Appl
30	86	85.1	140	3 US-08-569-147-82	Sequence 82, Appl
31	86	85.1	365	3 US-08-875-811-53	Sequence 53, Appl
32	86	85.1	366	3 US-08-875-811-55	Sequence 55, Appl
33	85	84.2	136	3 US-09-184-658-32	Sequence 32, Appl
34	85	84.2	136	4 US-09-504-262D-32	Sequence 32, Appl
35	85	84.2	259	4 US-09-419-788-115	Sequence 115, App
36	85	84.2	278	4 US-09-184-658-47	Sequence 47, Appl
37	85	84.2	278	4 US-09-504-262D-47	Sequence 47, Appl
38	85	84.2	284	3 US-09-504-262D-40	Sequence 40, Appl
39	85	84.2	284	4 US-09-504-262D-40	Sequence 40, Appl
40	84	83.2	119	4 US-09-232-290-50	Sequence 50, Appl
41	83	82.2	118	1 US-08-425-336-126	Sequence 126, App
42	83	82.2	118	1 US-08-488-113B-126	Sequence 126, App
43	83	82.2	118	1 US-08-477-484B-126	Sequence 126, App
44	83	82.2	118	1 US-08-107-669D-67	Sequence 67, Appl
45	83	82.2	118	1 US-08-472-788A-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1  
US-09-318-786-35  
; Sequence 35, Application US/09318786  
; Patent No. 6472147  
; GENERAL INFORMATION:  
; APPLICANT: Janda, Kim D  
; APPLICANT: Wirsching, Peter  
; APPLICANT: Lerner, Richard A  
; APPLICANT: Gao, Changshou  
; TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON  
; TITLE OF INVENTION: FILAMENTOUS PHAGE USING PY11 AND PIX, COMPOSITIONS,  
; TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES  
; FILE REFERENCE: TSR0305  
; CURRENT APPLICATION NUMBER: US/09/318,786  
; CURRENT FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: fusion  
US-09-318-786-35

Query Match 90.1%; Score 91; DB 4; Length 160;  
Best Local Similarity 88.2%; Pred. No. 2.9e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
Db 52 WINTYTGPTYADDFRG 68

RESULT 2  
US-08-279-772A-6  
; Sequence 6, Application US/08279772A  
; Patent No. 6080560  
; GENERAL INFORMATION:  
; APPLICANT: Russell, David R  
; APPLICANT: Fuller, James T  
; TITLE OF INVENTION: Method for Producing Antibodies in Plant  
; TITLE OF INVENTION: Cells  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles and Brady  
; STREET: PO Box 2113  
; CITY: Madison  
; STATE: WI



COUNTRY: United States of America  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/279,772A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9097-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-279-772A-6

Query Match 90.1%; Score 91; DB 3; Length 252;  
Best Local Similarity 88.2%; Pred. No. 4.7e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||:|||||  
DB 180 WINTYTGPTYADDFKG 196

RESULT 3  
US-08-902-486-9  
Sequence 9, Application US/08902486  
Patent No. 6140075  
GENERAL INFORMATION:  
APPLICANT: Russel, David R.  
APPLICANT: Fuller, James T.  
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND  
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,486  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 670513.90261  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-902-486-9

Query Match 90.1%; Score 91; DB 3; Length 252;  
Best Local Similarity 88.2%; Pred. No. 4.7e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||:|||||  
DB 180 WINTYTGPTYADDFKG 196

RESULT 4  
US-08-425-336-124  
Sequence 124, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Stuchlika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-124

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||:|||||  
DB 50 WINTYTGPTYADDFKG 66



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RESULT 5
US-08-488-113B-124
; Sequence 124, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-124

Query Match      88.1%; Score 89; DB 1; Length 118;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 WINTYTGPTYAGDFKG 17
      ||||:|||||
Db      50 WINTHTGPTYADDFKG 66

RESULT 6
US-08-477-484B-124
; Sequence 124, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-124

Query Match      88.1%; Score 89; DB 1; Length 118;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 WINTYTGPTYAGDFKG 17
      ||||:|||||
Db      50 WINTHTGPTYADDFKG 66

RESULT 7
US-08-107-669D-28
; Sequence 28, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
```

STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
FILING DATE: 13-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-28

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
||||:|||||  
Db 50 WINTHTGEPYADDFKG 66

## RESULT 8

US-08-107-669D-29  
Sequence 29, Application US/08107669D  
Patent No. 5766886  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
FILING DATE: 13-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-29

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
||||:|||||  
Db 50 WINTHTGEPYADDFKG 66

## RESULT 9

US-08-107-669D-66  
Sequence 66, Application US/08107669D  
Patent No. 5766886  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
FILING DATE: 13-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-66

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
| | | | : | | | | | | | | | |  
Db 50 WINTHTGPTYADDFKG 66

## RESULT 10

US-08-472-788A-28  
; Sequence 28, Application US/08472788A  
; Patent No. 5770196  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,788A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/082,842  
; FILING DATE: 23-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 0610.1000003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/371-2600  
; TELEFAX: 202/371-2540  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-472-788A-28

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
| | | | : | | | | | | | | | |  
Db 50 WINTHTGPTYADDFKG 66

## RESULT 11

US-08-472-788A-29  
; Sequence 29, Application US/08472788A  
; Patent No. 5770196  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-788A-29

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
| | | | : | | | | | | | | | |  
Db 50 WINTHTGPTYADDFKG 66

## RESULT 12

US-08-472-788A-88  
; Sequence 88, Application US/08472788A  
; Patent No. 5770196  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,788A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
US-08-472-788A-88

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
||||:|||||  
Db 50 WINTHTGPTYADDFKG 66

RESULT 13  
US-08-477-531B-28  
Sequence 28, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
US-08-477-531B-28

Query Match 88.1%; Score 89; DB 2; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
||||:|||||  
Db 50 WINTHTGPTYADDFKG 66

RESULT 14  
US-08-477-531B-29  
Sequence 29, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
US-08-477-531B-29

Query Match 88.1%; Score 89; DB 2; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
||||:|||||  
Db 50 WINTHTGPTYADDFKG 66

## RESULT 15

US-08-477-531B-66

; Sequence 66, Application US/08477531B  
; Patent No. 5821123

; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: United States of America

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,531B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/107,669

; FILING DATE: 13-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/10906

; FILING DATE: 14-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/808,464

; FILING DATE: 13-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Michele A. Cimbalà

; REGISTRATION NUMBER: 33,851

; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202/371-2600

; TELEFAX: 202/371-2540

; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 118 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-477-531B-66

Query Match 88.1%; Score 89; DB 2; Length 118;

Best Local Similarity 88.2%; Pred.No. 4.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
||||:|||||

Db 50 WINTHTGPTYADDFKG 66

Search completed: March 1, 2005, 17:46:55  
Job time : 33.2154 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 91.0154 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-16  
Perfect score: 101  
Sequence: 1 WINTYTGPTYAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	14	US-10-071-962-16
2	94	93.1	17	10	US-09-791-551-86
3	94	93.1	17	16	US-10-018-245A-2
4	94	93.1	67	14	US-10-243-130-19
5	94	93.1	70	14	US-10-243-130-17
6	94	93.1	70	14	US-10-243-130-18
7	94	93.1	112	15	US-10-383-447-10
8	94	93.1	112	15	US-10-383-447-18
9	94	93.1	116	14	US-10-138-727A-2
10	94	93.1	116	14	US-10-138-727A-18
11	94	93.1	116	14	US-10-138-727A-19
12	94	93.1	116	14	US-10-138-727A-20
13	94	93.1	116	14	US-10-138-727A-21

14	94	93.1	116	14	US-10-138-727A-22	Sequence 22, Appl
15	94	93.1	116	14	US-10-138-727A-23	Sequence 23, Appl
16	94	93.1	116	14	US-10-138-727A-24	Sequence 24, Appl
17	94	93.1	116	14	US-10-138-727A-25	Sequence 25, Appl
18	94	93.1	116	14	US-10-138-727A-26	Sequence 26, Appl
19	94	93.1	116	14	US-10-310-719-30	Sequence 30, Appl
20	94	93.1	116	14	US-10-310-719-33	Sequence 33, Appl
21	94	93.1	116	15	US-10-468-370-658	Sequence 658, App
22	94	93.1	116	15	US-10-468-370-660	Sequence 660, App
23	94	93.1	116	15	US-10-468-370-662	Sequence 662, App
24	94	93.1	116	15	US-10-468-370-664	Sequence 664, App
25	94	93.1	116	15	US-10-468-370-666	Sequence 666, App
26	94	93.1	116	15	US-10-468-370-668	Sequence 668, App
27	94	93.1	116	15	US-10-468-370-670	Sequence 670, App
28	94	93.1	116	15	US-10-468-370-672	Sequence 672, App
29	94	93.1	116	16	US-10-468-496-2021	Sequence 2021, Ap
30	94	93.1	116	16	US-10-468-496-2023	Sequence 2023, Ap
31	94	93.1	116	16	US-10-468-496-2025	Sequence 2025, Ap
32	94	93.1	116	16	US-10-468-496-2027	Sequence 2027, Ap
33	94	93.1	116	16	US-10-468-496-2029	Sequence 2029, Ap
34	94	93.1	116	16	US-10-468-496-2031	Sequence 2031, Ap
35	94	93.1	116	16	US-10-468-496-2033	Sequence 2033, Ap
36	94	93.1	116	16	US-10-468-496-2035	Sequence 2035, Ap
37	94	93.1	117	14	US-10-138-727A-35	Sequence 35, Appl
38	94	93.1	117	14	US-10-422-049-20	Sequence 20, Appl
39	94	93.1	118	14	US-10-422-049-19	Sequence 19, Appl
40	94	93.1	119	14	US-10-269-010-1	Sequence 1, Appli
41	94	93.1	119	14	US-10-268-883-3	Sequence 3, Appli
42	94	93.1	138	14	US-10-268-883-2	Sequence 2, Appli
43	94	93.1	139	10	US-09-791-551-113	Sequence 113, App
44	94	93.1	579	14	US-10-138-727A-41	Sequence 41, Appl
45	94	93.1	579	14	US-10-310-719-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-10-071-962-16  
; Sequence 16, Application US/10071962  
; Publication No. US20030170237A1  
; GENERAL INFORMATION:  
; APPLICANT: BauFu Ni  
; APPLICANT: Bill N.C. Sun  
; APPLICANT: Cedily R.Y. Sun  
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
; FILE REFERENCE: 98-3 Screening Method Therefor  
; CURRENT APPLICATION NUMBER: US/10/071,962  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US/09/303,155A  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/083,575  
; PRIOR FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: mouse  
; US-10-071-962-16

Query Match 100.0%; Score 101; DB 14; Length 17;  
Best local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
Db 1 WINTYTGPTYAGDFKG 17

RESULT 2  
US-09-791-551-86

; Sequence 86, Application US/09791551  
; Publication No. US20030235584A1  
; GENERAL INFORMATION:  
; APPLICANT: KLOETZER, WILLIAM S.  
; APPLICANT: HANNA, NABIL  
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
; FILE REFERENCE: 037003/027869  
; CURRENT APPLICATION NUMBER: US/09/791,551  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/185,390  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/233,625  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 86  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-791-551-86

Query Match 93.1%; Score 94; DB 10; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYTGPTYAGDFKG 17  
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DB 1 WINTYTGPTYADDFKG 17

## RESULT 3

US-10-018-245A-2  
; Sequence 2, Application US/10018245A  
; Publication No. US20040115196A1  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Yoshiaki  
; APPLICANT: NAGAHIRA, Kazuhiro  
; APPLICANT: NAKANISHI, Toshihiro  
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complemen  
; TITLE OF INVENTION: determining regions and genes encoding the same  
; FILE REFERENCE: 46224  
; CURRENT APPLICATION NUMBER: US/10/018,245A  
; CURRENT FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: JP 117394/2000  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: mouse  
; FEATURE:  
; OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody  
US-10-018-245A-2

Query Match 93.1%; Score 94; DB 16; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYTGPTYAGDFKG 17  
|||  
DB 1 WINTYTGPTYADDFKG 17

## RESULT 4

US-10-243-130-19  
; Sequence 19, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sabs, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED

; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-10-243-130-19

Query Match 93.1%; Score 94; DB 14; Length 67;  
Best Local Similarity 94.1%; Pred. No. 5.4e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYTGPTYAGDFKG 17  
|||  
DB 44 WINTYTGPTYADDFKG 60

## RESULT 5

US-10-243-130-17  
; Sequence 17, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sabs, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED  
; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-243-130-17

Query Match 93.1%; Score 94; DB 14; Length 70;  
Best Local Similarity 94.1%; Pred. No. 5.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYTGPTYAGDFKG 17  
|||  
DB 47 WINTYTGPTYADDFKG 63

## RESULT 6

US-10-243-130-18  
; Sequence 18, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sabs, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED  
; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-130-18
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Query Match          93.1%; Score 94; DB 14; Length 70;
Best Local Similarity 94.1%; Pred. No. 5.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 WINTYTGEPYAGDFKG 17
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Db       47 WINTYTGEPYADDFKG 63
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## RESULT 7

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US-10-383-447-10
; Sequence 10, Application US/10383447
; Publication No. US20040096392A1
; GENERAL INFORMATION:
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; APPLICANT: Bhaskar, Vinay
; APPLICANT: de la Calle, Agustin
; APPLICANT: Law, Debbie
; APPLICANT: Caras, Ingrid
; APPLICANT: Ramakrishnan, Vanitha
; APPLICANT: Murray, Richard
; APPLICANT: Afar, Daniel
```

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; TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
; FILE REFERENCE: 05882.0138.NPUS00
; CURRENT APPLICATION NUMBER: US/10/383,447
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/362,837
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 60/463,812
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
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; OTHER INFORMATION: Heavy chain variable region
US-10-383-447-10
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Query Match          93.1%; Score 94; DB 15; Length 112;
Best Local Similarity 94.1%; Pred. No. 9.2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 WINTYTGEPYAGDFKG 17
         |||||
Db       50 WINTYTGEPYADDFKG 66
```

## RESULT 8

```
US-10-383-447-18
; Sequence 18, Application US/10383447
; Publication No. US20040096392A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bhaskar, Vinay
; APPLICANT: de la Calle, Agustin
; APPLICANT: Law, Debbie
; APPLICANT: Caras, Ingrid
; APPLICANT: Ramakrishnan, Vanitha
; APPLICANT: Murray, Richard
; APPLICANT: Afar, Daniel
```

```
; APPLICANT: Powers, David
; TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
; FILE REFERENCE: 05882.0138.NPUS00
; CURRENT APPLICATION NUMBER: US/10/383,447
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
```

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; PRIOR APPLICATION NUMBER: US 60/362,837
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 60/463,812
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
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; OTHER INFORMATION: Heavy chain variable region
US-10-383-447-18
```

```
Query Match          93.1%; Score 94; DB 15; Length 112;
Best Local Similarity 94.1%; Pred. No. 9.2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 WINTYTGEPYAGDFKG 17
         |||||
Db       50 WINTYTGEPYADDFKG 66
```

## RESULT 9

```
US-10-138-727A-2
; Sequence 2, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Susan
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/10/138,727A
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
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```
; OTHER INFORMATION: KS VH mouse
US-10-138-727A-2
```

```
Query Match          93.1%; Score 94; DB 14; Length 116;
Best Local Similarity 94.1%; Pred. No. 9.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WINTYTGEPYAGDFKG 17
         |||||
Db       50 WINTYTGEPYADDFKG 66
```

## RESULT 10

```
US-10-138-727A-18
; Sequence 18, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Susan
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/10/138,727A
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
```

; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VH7 heavy chain  
US-10-138-727A-18

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 11  
US-10-138-727A-19

; Sequence 19, Application US/10138727A  
; Publication No. US20030157054A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Susan  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/10/138,727A  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 19  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VH2.5 heavy chain  
US-10-138-727A-19

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 12  
US-10-138-727A-20

; Sequence 20, Application US/10138727A  
; Publication No. US20030157054A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Susan  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/10/138,727A  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 20  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: KS VH veneered  
US-10-138-727A-20

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 13  
US-10-138-727A-21

; Sequence 21, Application US/10138727A  
; Publication No. US20030157054A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Susan  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/10/138,727A  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 21  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: KS de-immunized VH1  
US-10-138-727A-21

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 14  
US-10-138-727A-22

; Sequence 22, Application US/10138727A  
; Publication No. US20030157054A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Susan  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/10/138,727A  
; CURRENT FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 22  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: KS de-immunized VH2  
US-10-138-727A-22

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||  
Db 50 WINTYTGEPYADDFKG 66



RESULT 15

US-10-138-727A-23

; Sequence 23, Application US/10138727A  
; Publication No. US20030157054A1

; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen

; APPLICANT: Lo, Kin-Ming

; APPLICANT: Qian, Susan

; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

; FILE REFERENCE: LEX-019

; CURRENT APPLICATION NUMBER: US/10/138,727A

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US 60/288,564

; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 23

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: KS de-immunized VH3

US-10-138-727A-23

Query Match 93.1%; Score 94; DB 14; Length 116;

Best Local Similarity 94.1%; Pred. No. 9.5e-07;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPTYAGDFKG 17

Db 50 WINTYTGEPTYADDFKG 66

Search completed: March 1, 2005, 17:52:49  
Job time : 91.0154 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 23.0154 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-16  
Perfect score: 101  
Sequence: 1 WINTYTGEPYAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	94	93.1	101	2	D24672	Ig heavy chain V r
2	94	93.1	105	2	S24764	Ig heavy chain V r
3	94	93.1	105	2	S24765	Ig heavy chain V r
4	94	93.1	109	2	S26325	Ig heavy chain V r
5	94	93.1	118	2	S19967	Ig heavy chain V r
6	94	93.1	119	2	A53285	Ig heavy chain V a
7	94	93.1	124	2	PH1404	Ig heavy chain V r
8	91	90.1	115	2	S19968	Ig heavy chain V r
9	91	90.1	120	2	B42848	I6 mAb heavy chain
10	91	90.1	146	4	S33905	Ig heavy chain pre
11	90	89.1	102	2	C32530	Ig heavy chain V r
12	85	84.2	105	2	S24766	Ig heavy chain V r
13	84	83.2	118	2	A32530	Ig heavy chain V r
14	83	82.2	114	2	D32967	Ig heavy chain V r
15	83	82.2	114	2	C32967	Ig heavy chain V r
16	83	82.2	117	2	S32187	Ig heavy chain V r
17	83	82.2	117	2	S32190	Ig heavy chain V r
18	82	81.2	115	2	S19965	Ig heavy chain V r
19	82	81.2	136	2	S35759	BHD9D10 protein -
20	81	80.2	119	2	B32530	Ig heavy chain V r
21	80	79.2	93	2	C24672	Ig heavy chain V r
22	80	79.2	99	2	S26326	Ig heavy chain V r
23	79.5	78.7	119	2	H45722	anti-glycoprotein
24	79	78.2	113	2	B36259	Ig heavy chain V r
25	79	78.2	114	2	PL0256	Ig heavy chain V r
26	79	78.2	120	2	S19963	Ig heavy chain V r
27	79	78.2	139	2	PH1225	Ig heavy chain pre
28	73	72.3	120	2	S26789	Ig heavy chain V r
29	71	70.3	98	2	S46460	Ig heavy chain V r

30	71	70.3	118	2	S37204	Ig heavy chain V r
31	66	65.3	98	2	A49051	Ig heavy chain V7
32	66	65.3	105	2	S24763	Ig heavy chain V r
33	66	65.3	117	2	S18554	Ig heavy chain V r
34	66	65.3	131	2	S26792	Ig heavy chain V r
35	62	61.4	142	2	S19245	Ig heavy chain pre
36	61	60.4	98	2	H34964	Ig heavy chain V-I
37	58	57.4	134	2	S21916	Ig heavy chain V r
38	52	51.5	86	2	S54912	Ig heavy chain V r
39	49	48.5	229	2	T18605	hypothetical prote
40	47	46.5	98	2	PH0871	Ig heavy chain V r
41	47	46.5	181	2	S21924	Ig heavy chain V r
42	47	46.5	160	2	PL0105	anti-PR2 erythrocy
43	47	46.5	789	2	F71161	probable chemotacti
44	46.5	46.0	6486	2	T31076	tyrocidine synthe
45	46	45.5	79	2	A49021	Ig heavy chain V-X

ALIGNMENTS

RESULT 1  
D24672  
Ig heavy chain V region (VGAM3-8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999  
C/Accession: D24672  
R/Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985  
A/Reference number: A91022; MUID:86055722; PMID:2998759  
A/Accession: D24672  
A/Molecule type: DNA  
A/Residues: 1-101 <WIN>  
A/Cross-references: GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:g773215  
A/Note: this sequence was determined from the differentiated gene  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 93.1%; Score 94; DB 2; Length 101;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
Db 31 WINTYTGEPYADDFKG 47

RESULT 2  
S24764  
Ig heavy chain V region (subgroup XI) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C/Accession: S24764; S24772; S24777  
R/Klaes, S.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24763  
A/Accession: S24764  
A/Molecule type: DNA  
A/Residues: 1-105 <KLA>  
A/Cross-references: EMBL:Z14999  
A/Accession: S24772  
A/Molecule type: DNA  
A/Residues: 1-105 <KLW>  
A/Cross-references: EMBL:Z15011  
R/Thomas, J.W.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24775  
A/Accession: S24777  
A/Molecule type: DNA  
A/Residues: 1-105 <THO>  
A/Cross-references: EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID:g52617  
C/Genetics:  
A;Introns: 9/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 105;  
Best Local Similarity 94.1%; Pred. No. 1.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||  
Db 62 WINTYTGPTYADDFKG 78

RESULT 3

S24765 Ig heavy chain V region (subgroup XI) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C;Accession: S24765; S24773; S24778

R;Klages, S.  
submitted to the EMBL Data Library, August 1992

A;Reference number: S24763

A;Accession: S24765

A;Molecule type: DNA

A;Residues: 1-105 <KLA>

A;Cross-references: EMBL:Z15001

A;Accession: S24773

A;Molecule type: DNA

A;Residues: 1-105 <KLW>

A;Cross-references: EMBL:Z15013

R;Thomas, J.W.  
submitted to the EMBL Data Library, August 1992

A;Reference number: S24776

A;Accession: S24778

A;Molecule type: DNA

A;Residues: 1-105 <THO>

A;Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620

C;Genetics: 9/1

A;introns: 9/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 105;  
Best Local Similarity 94.1%; Pred. No. 1.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||  
Db 62 WINTYTGPTYADDFKG 78

RESULT 4

S26325 Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S26325

R;Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991

A;Title: Antibodies that are specific for a single amino acid interchange in a protein

A;Reference number: S26309; MUID:91314121; PMID:1908510

QY 1 WINTYTGPTYAGDFKG 17  
|||||  
Db 40 WINTYTGPTYADDFKG 56

RESULT 5

S19967 Ig heavy chain V region (M-T406) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S19967

R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19967

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-118 <WEI>

A;Cross-references: UNIPROT:Q921A6; EMBL:X65090

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; Length 118;  
Best Local Similarity 94.1%; Pred. No. 1.9e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||  
Db 47 WINTYTGPTYADDFKG 63

RESULT 6

A53285 Ig heavy chain V and J regions, monoclonal antibody SCET.M8.1 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C;Accession: A53285

R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
Mol. Immunol. 28, 1063-1072, 1991

A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct

A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBIIP:63299)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; Length 119;  
Best Local Similarity 94.1%; Pred. No. 2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|||||  
Db 50 WINTYTGPTYADDFKG 66

RESULT 7

PH1404 Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000

C;Accession: PH1404; PH1406

R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tai

J. Exp. Med. 176, 1209-1214, 1992

A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t

A;Reference number: PH1403; MUID:93018837; PMID:1402663

A;Accession: PH1404

A;Molecule type: DNA

A;Residues: 1-124 <SH1>

A;Accession: PH1406

A;Molecule type: DNA

A;Residues: 115-121 <SH2>

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

F;35-118/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; length 124;  
Best Local Similarity 94.1%; Pred. No. 2e-07;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17

Db 70 WINTYTGEPYADDFKG 86

#### RESULT 8

S19968

Ig heavy chain V region (M-T408) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S19968

R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A;Description: Structural characterization of CD4 mAb.

A;Reference number: S19963

A;Accession: S19968

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <WEI>

A;Cross-references: UNIPROT:Q921A6; EMBL:X65089

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 91; DB 2; length 115;  
Best Local Similarity 88.2%; Pred. No. 5.5e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17

Db 45 WINTYTGQPTYADDFKG 61

#### RESULT 9

B42848

L6 mAb heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C;Accession: B42848; S33903

R;Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo

J. Biol. Chem. 267, 15552-15558, 1992

A;Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character

A;Reference number: A42848; MUID:92348410; PMID:1639794

A;Accession: B42848

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-120 <FEL>

A;Cross-references: GB:M90690; NID:g195065; PIDN:AAA38146.1; PID:g195066

A;Note: sequence extracted from NCBI backbone (NCBI:109960, NCBI:P.109961)

A;Accession: S33903

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <FE2>

A;Cross-references: EMBL:M90691

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 91; DB 2; length 120;  
Best Local Similarity 88.2%; Pred. No. 5.8e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17

Db 50 WINTYTGQPTYADDFKG 66

#### RESULT 10

S33905

Ig heavy chain precursor V region - synthetic

C;Species: synthetic

C;Date: 13-Jan-1995 #sequence\_revision 30-Apr-1998 #text\_change 20-Oct-2000

C;Accession: S33905

R;Liu, A.Y.; Robinson, R.R.; Hellstroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstroem

Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987

A;Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.

A;Reference number: S33905; MUID:87204152; PMID:3106970

A;Accession: S33905

A;Molecule type: mRNA

A;Residues: 1-146 <LIU>

A;Cross-references: EMBL:M6072; NID:g195270; PIDN:AAA38229.1; PID:g195271

Query Match 90.1%; Score 91; DB 4; length 146;  
Best Local Similarity 88.2%; Pred. No. 7.1e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17

Db 69 WINTYTGQPTYADDFKG 85

#### RESULT 11

C32530

Ig heavy chain V region (10/8) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 16-Aug-1996

C;Accession: C32530

R;Deverson, E.; Berek, C.; Tausig, M.; Feinstein, A.

Eur. J. Immunol. 17, 9-13, 1987

A;Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region he

A;Reference number: A32530; MUID:87133855; PMID:3102254

A;Accession: C32530

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-102 <DEV>

A;Cross-references: GB:M27585

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 90; DB 2; length 102;  
Best Local Similarity 88.2%; Pred. No. 7e-07;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17

Db 33 WINTYTGEPYTDDFKG 49

#### RESULT 12

S24766

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C;Accession: S24766; S24774; S24779

R;Klages, S.

submitted to the EMBL Data Library, August 1992

A;Reference number: S24763

A;Accession: S24766

A;Molecule type: DNA

A;Residues: 1-105 <KLA>





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 110.108 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-16  
Perfect score: 101  
Sequence: 1 WINTYTGPTVAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	93.1	241	2 Q921A6	Q921A6 mus musculu
2	85	84.2	102	2 Q9JL79	Q9JL79 mus musculu
3	80	79.2	116	2 Q683Y7	Q683Y7 mus musculu
4	80	79.2	116	2 Q683Y8	Q683Y8 mus musculu
5	79	78.2	140	2 Q65ZL3	Q65ZL3 mus sp. tgl
6	71	70.3	125	2 Q6PIL0	Q6PIL0 homo sapien
7	67	66.3	218	2 Q925S1	Q925S1 mus musculu
8	65	64.4	484	2 Q99LA6	Q99LA6 mus musculu
9	56	55.4	1549	2 Q76D19	Q76D19 clostridium
10	49	48.5	229	2 Q9XUA0	Q9XUA0 caenorhabdi
11	49	48.5	763	1 THED CORGL	Q8nqh1 c multifunc
12	48	47.5	600	2 Q9B096	Q9B096 mycobacteri
13	47	46.5	192	2 Q8PCD7	Q8pcd7 xanthomonas
14	47	46.5	322	2 Q857U4	Q857U4 mycobacteri
15	47	46.5	732	2 Q6LNG6	Q6lng6 photobacter
16	47	46.5	739	2 Q58227	Q58227 pyrococcus
17	47	46.5	2151	2 Q6B7Y9	Q6b7y9 suchong vir
18	47	46.5	3399	2 Q6LTY5	Q6lt25 photobacter
19	46.5	46.0	6486	1 TYCC BREPA	Q30409 b tyrocidin
20	46	45.5	150	1 GRDA CLOPU	P26970 clostridium
21	46	45.5	379	2 Q87GI8	Q87gi8 vibrio para
22	46	45.5	500	2 Q6N091	Q6n091 homo sapien
23	46	45.5	598	2 Q857J4	Q857j4 mycobacteri
24	46	45.5	617	2 Q8Y6K6	Q8y6k6 listeria mo
25	46	45.5	617	2 Q92AY2	Q92ay2 listeria in
26	46	45.5	617	2 Q71YY9	Q71yy9 listeria mo
27	46	45.5	618	2 Q9KCE2	Q9kce2 bacillus ha
28	46	45.5	739	1 THED COREF	Q8ftn8 c multifunc
29	46	45.5	739	2 Q8JVD0	Q8jvd0 foot-and-mo
30	45	44.6	389	2 Q752V2	Q752v2 ashbya goss
31	45	44.6	411	2 Q6PPG2	Q6ppg2 chlamydomon

32	45	44.6	419	2 Q6IO97	Q6ig97 brachydanio
33	45	44.6	419	2 Q7ZV02	Q7zv02 brachydanio
34	45	44.6	469	2 Q7Z7P5	Q7z7p5 homo sapien
35	45	44.6	487	2 Q6QBS6	Q6qbs6 chlamydomon
36	45	44.6	518	2 Q6N030	Q6n030 homo sapien
37	45	44.6	585	2 Q6UE12	Q6ue12 lactobacill
38	45	44.6	591	2 Q74JU8	Q74ju8 lactobacill
39	45	44.6	614	2 Q8DX11	Q8dx11 streptococc
40	45	44.6	614	2 Q8E2W0	Q8e2w0 streptococc
41	45	44.6	839	2 Q19198	Q19198 caenorhabdi
42	45	44.6	842	2 Q65ZH7	Q65zh7 caenorhabdi
43	45	44.6	868	2 Q8A2M9	Q8a2m9 bacteroides
44	45	44.6	2009	2 Q7N848	Q7n848 photorhabdu
45	44.5	44.1	309	2 Q8R7D4	Q8r7d4 thermoanaer

ALIGNMENTS

RESULT 1

ID Q921A6 PRELIMINARY; PRT; 241 AA.  
AC Q921A6; (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE Anti-CEA 79 single chain Fv (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98170165; PubMed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scFv).";  
RL Mol. Cells 7:816-819(1997).  
DR EMBL; U88067; AAB48044.1; -.  
DR PIR; S19965; S19965.  
DR PIR; S19967; S19967.  
DR PIR; S19968; S19968.  
DR PIR; S26325; S26325.  
DR HSSP; P01607; 1BMW.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 241  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 93.1%; Score 94; DB 2; Length 241;  
Best local Similarity 94.1%; Pred. No. 5.8e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTVAGDFKG 17  
Db 50 WINTYTGPTVADDFKG 66

RESULT 2

ID Q9JL79 PRELIMINARY; PRT; 102 AA.  
AC Q9JL79;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)  
DE Anti-myosin immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992448;
DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206027; AAF69325.1; -.
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 11543 MW; ES90C292093F6711 CRC64;
```

```
Query Match 84.2%; Score 85; DB 2; Length 102;
Best Local Similarity 88.2%; Pred. No. 6.8e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 WINTYTGEPYAGDFKG 17
    |||||
Db 35 WINTETGEPYADDFKG 51
```

## RESULT 3

```
Q683Y7 PRELIMINARY; PRT; 116 AA.
```

```
ID Q683Y7
AC Q683Y7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
```

```
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Balb/c;
```

```
RA Phalipon A., Costachel C., Thuizat A., Nato F.;
```

```
RT "Anti-11popolysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen."
```

```
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
```

```
DR EMBL; AJ784033; CAH04483.1; -.
```

```
DR InterPro; IPR003599; Ig.
```

```
DR InterPro; IPR007110; Ig-1like.
```

```
DR InterPro; IPR003596; Ig_v.
```

```
DR Pfam; PF00047; Ig_1.
```

```
DR SMART; SM00409; IGV; 1.
```

```
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PSS0835; IG_LIKE; 1.
```

```
FT NON_TER 1
```

```
FT NON_TER 116
```

```
SQ SEQUENCE 116 AA; 12863 MW; 5EC1AD02E911952 CRC64;
```

```
Query Match 79.2%; Score 80; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 5.1e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 WINTYTGEPYAGDFKG 17
    |||||
Db 50 WINTETGEPYADDFKG 66
```

## RESULT 4

```
Q683Y8 PRELIMINARY; PRT; 116 AA.
```

```
ID Q683Y8
```

```
AC Q683Y8;
```

```
DT 25-OCT-2004 (TREMBLrel. 28, Created)
```

```
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
```

```
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
```

```
DE Immunoglobulin heavy chain variable region (Fragment).
```

```
GN Name=IGHV;
```

```
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10090;
```

```
RN [1]
```

```
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Balb/c;
```

```
RA Phalipon A., Costachel C., Thuizat A., Nato F.;
```

```
RT "Anti-11popolysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen."
```

```
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
```

```
DR EMBL; AJ784032; CAH04482.1; -.
```

```
DR InterPro; IPR003599; Ig.
```

```
DR InterPro; IPR007110; Ig-1like.
```

```
DR InterPro; IPR003596; Ig_v.
```

```
DR SMART; SM00409; IGV; 1.
```

```
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PSS0835; IG_LIKE; 1.
```

```
FT NON_TER 1
```

```
FT NON_TER 116
```

```
SQ SEQUENCE 116 AA; 12833 MW; C85932C0D843778D CRC64;
```

```
Query Match 79.2%; Score 80; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 5.1e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 WINTYTGEPYAGDFKG 17
    |||||
Db 50 WINTATGEPYPDDFKG 66
```

## RESULT 5

```
Q65ZL3 PRELIMINARY; PRT; 140 AA.
```

```
ID Q65ZL3
```

```
AC Q65ZL3;
```

```
DT 25-OCT-2004 (TREMBLrel. 28, Created)
```

```
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
```

```
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
```

```
DE Tg10H (Fragment).
```

```
GN Name=Tg10H;
```

```
OS Mus sp.
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10095;
```

```
RN [1]
```

```
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;
```

```
RA Noel D., Bernardi T., Navarro-Teulon I., Marin M., Martinetto J.P.,
```

```
RA Ducancel F., Mani J.C., Pau B., Plechaczkyk M., Biard-Plechaczkyk M.;
```

```
RT "Analysis of the individual contributions of immunoglobulin heavy and
```

```
RT light chains to the binding of antigen using cell transfection and
```

```
RT plasmon resonance analysis."
```

```
RL J. Immunol. Methods 193:177-187(1996).
```

```
DR EMBL; S82492; AAB37434.2; -.
```

```
DR InterPro; IPR003599; Ig.
```

```
DR InterPro; IPR007110; Ig-1like.
```

```
DR InterPro; IPR003596; Ig_v.
```

```
DR SMART; SM00409; IGV; 1.
```

```
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PSS0835; IG_LIKE; 1.
```

```
FT NON_TER 140
```

```
FT NON_TER 140
```

```
SQ SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965FA3 CRC64;
```

```
Query Match 78.2%; Score 79; DB 2; Length 140;
```

Best Local Similarity 76.5%; Pred. No. 9e-05;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WINTYTGPTVAGDFKG 17  
||||:|||||  
Db 69 WINTFSGVPTVADDFKG 85

RESULT 6

Q6PIL0 PRELIMINARY; PRT; 125 AA.  
AC Q6PIL0;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC032733; AAH32733.1; -.  
DR HSSP; P01751; 1A6W.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Hypothetical protein.

QY SEQUENCE 125 AA; 13913 MW; B76CE434F5A69788 CRC64;  
Query Match 70.3%; Score 71; DB 2; Length 125;  
Best Local Similarity 70.6%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WINTYTGPTVAGDFKG 17  
||||:|||||  
Db 69 WNTYTGNTPTVAGDFTG 85

RESULT 7

Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL; AF240168; AAK43733.1; -.  
DR HSSP; P01665; 1QNZ.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FABF7982817 CRC64;  
Query Match 66.3%; Score 67; DB 2; Length 218;  
Best Local Similarity 64.7%; Pred. No. 0.013;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WINTYTGPTVAGDFKG 17  
||||:|||||  
Db 52 WINTHSGVTPKVAEEFKG 68

RESULT 8

Q99LA6 PRELIMINARY; PRT; 484 AA.  
AC Q99LA6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human



RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003495; AA03495.1; -.  
DR PIR; F33932; F33932.  
DR PIR; S19963; S19963.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 484 AA; 52567 MW; 8EAE4F9BCF582FA CRC64;

Query Match 64.4%; Score 65; DB 2; Length 484;  
Best Local Similarity 64.7%; Pred. No. 0.064;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|:| ||| ||| |||  
Db 69 WVNIEGTGESVYADDFKG 85

RESULT 9  
ID Q76D19 PRELIMINARY; PRT; 1549 AA.  
AC Q76D19;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Beta-N-acetylglucosaminidase (EC 3.2.1.52).  
GN Name=nag84A;  
OS Clostridium paraputrificum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=29363;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li H., Morimoto K., Kimura T., Sakka K., Lun S., Ohmiya K.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by  
CC an amide bond (By similarity).  
DR EMBL; AB109099; BAC99989.1; -.  
DR GO; GO:0009986; C:cell surface; IEA.  
DR GO; GO:0004563; F:beta-N-acetylhexosaminidase activity; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR000421; FA58\_C.  
DR InterPro; IPR011490; FIVAR.  
DR InterPro; IPR001899; Gram\_pos\_anchor.  
DR InterPro; IPR011496; Hyal\_ase.  
DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
DR Pfam; PF07554; FIVAR; 2.  
DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR Pfam; PF07555; Hyaluronidase\_2; 1.  
DR TIGRFAMs; TIGR01167; LPXTG\_anchor; 1.  
DR PROSITE; PS50022; FA58C\_3; 1.  
KW Cell wall; Glycosidase; Hydrolase; Peptidoglycan-anchor.  
SQ SEQUENCE 1549 AA; 174312 MW; C6AF8B2D96D47285 CRC64;

Query Match 55.4%; Score 56; DB 2; Length 1549;  
Best Local Similarity 58.8%; Pred. No. 6.5;  
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|:| ||| ||| |||  
Db 840 WYKTNDGDMTYAGDFVG 856

RESULT 10  
ID Q9XUA0 PRELIMINARY; PRT; 229 AA.  
AC Q9XUA0;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein AC8.7.  
GN ORFNames=AC8.7;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA McMurray A.A.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z83097; CAB05453.1; -.  
DR PIR; T18605; T18605.  
DR WormBase; WBGene00007079; AC8.7.  
DR WormPep; AC8.7; CE20441.  
KW Hypothetical protein.  
SQ SEQUENCE 229 AA; 26193 MW; 5520C31D3F1930C8 CRC64;

Query Match 48.5%; Score 49; DB 2; Length 229;  
Best Local Similarity 41.2%; Pred. No. 12;  
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 WINTYTGPTYAGDFKG 17  
|:| ||| ||| |||  
Db 31 WVRKIPGQKPYLGDYKG 47

RESULT 11  
ID THED\_CORGL STANDARD; PRT; 763 AA.  
AC Q8NQH1;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Multifunctional protein thIED [includes: Thiamine-phosphate  
DE pyrophosphorylase (EC 2.5.1.3) (TMP pyrophosphorylase) (TMP-Pase)  
DE (Thiamine-phosphate synthase); Phosphomethylpyrimidine kinase  
DE (EC 2.7.4.7) (HMP-phosphate kinase) (HMP-P kinase)].  
GN Name=thed; Synonyms=thidi; OrderedLocustNames=Cg11463, cg1654;  
OS Corynebacterium glutamicum (Brevibacterium flavum).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=1718;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
RA Nakagawa S.;  
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
RX PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;



OS	Mycobacteriophage Bxb1.
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX	NCBI_TaxID=148603;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20572070; PubMed=11123671;
RA	Mediavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R.,
RT	Hendrix R.W., Hatfull G.F.;
RL	"Genome organization and characterization of mycobacteriophage Bxb1.";
DR	Mol. Microbiol. 38:955-970(2000).
SQ	EMBL; AF271693; AAGS9730.1; -. F98F693F1BAECEB9 CRC64;
DB	SEQUENCE 600 AA; 66995 MW; P98F693F1BAECEB9 CRC64;
OY	2 INTYTGEPTTAGDF 15
	:           : :
Db	325 IDIYTG LPTPGEX 338
RESULT 13	
O8PCD7	
ID	O8PCD7 PRELIMINARY; PRT; 192 AA.
AC	O8PCD7;
DT	01-OCT-2002 (TReMBLrel. 22, Created)
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT	01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE	Hypothetical protein XCC0797.
CN	OrderedLocustNames=XCC0797;
OS	Xanthomonas campestris (pv. campestris).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC	Xanthomonadaceae; Xanthomonas.
OX	NCBI_TaxID=340;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 33913 / NCPPB 528;
RX	MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA	da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
RA	Quaggio R.B., Monteliro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA	Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA	Camarelle G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA	Cicarelli R.M.B., Coulinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA	Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA	Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA	Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA	Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA	Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA	Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA	Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA	Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA	Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA	Setubal J.C., Kitajima J.P.;
RT	"Comparison of the genomes of two Xanthomonas pathogens with differing
RT	host specificities.";
RL	Nature 417:459-463(2002).
DR	EMBL; AB012179; AAM40112.1; -.
KW	Complete proteome.
SQ	SEQUENCE 192 AA; 21202 MW; DDF149BC7EE01772 CRC64;
Query Match	46.5%; Score 47; DB 2; Length 192;
Best Local Similarity	56.2%; Pred. No. 21;
Matches 9; Conservative	1; Mismatches 6; Indels 0; Gaps 0;
OY	1 WINTYTGEPTTAGDFK 16
	:           :
Db	137 WISASVAEPTLAGWFK 152
RESULT 14	
O857U4	
ID	O857U4 PRELIMINARY; PRT; 322 AA.

AC Q857U4; 24, Created)  
DT 01-JUN-2003 (Tremblrel; 24, Last sequence update)  
DT 01-JUN-2003 (Tremblrel; 24, Last annotation update)  
DE Gp68.  
OS Mycobacteriophage Cjw1.  
OC Viruses; dsDNA viruses; no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=205869;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;  
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,  
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,  
RA Brucker W., Kumar V., Kandamany J., Keenan L., Bardarov S.,  
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
RA Hatfull G.F.;  
RT "Origins of highly mosaic mycobacteriophage genomes."  
RL Cell 113:171-182(2003)  
DR EMBL; AY129331; AAN01682.1; -  
SQ SEQUENCE 322 AA; 36011 MW; 96F4AA48392A2112 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 322;  
Best Local Similarity 56.2%; Pred. No. 36;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 INTYTGPTYAGDFK 17  
|||:|:|:|:|:|:|  
Db 93 INBYDGDPTYKGGDGG 108

RESULT 15

Q6LNQ6 PRELIMINARY; PRT; 732 AA.  
ID Q6LNQ6  
AC Q6LNQ6;  
DT 05-JUL-2004 (Tremblrel; 27, Created)  
DT 05-JUL-2004 (Tremblrel; 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel; 27, Last annotation update)  
DE Hypothetical protein VP0215.  
GN Name=VP0215; OrderedLocuSNames=BPRA2692;  
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Photobacterium.  
OX NCBI\_TaxID=74109;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,  
RA Valle G.;  
RT "Genome analysis of Photobacterium profundum reveals the complexity of  
RT high pressure adaptations."  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR378671; CAG21070.1; -  
DR InterPro; IPR010344; DUF940.  
DR Pfam; PF06082; DUF940; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 732 AA; 82241 MW; 2B59D15497B3DDF CRC64;

Query Match 46.5%; Score 47; DB 2; Length 732;  
Best Local Similarity 58.3%; Pred. No. 86;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 YTGPTYAGDFK 16  
|:|:|:|:|:|:|  
Db 95 YSGDPTFSGDTK 106

Search completed: March 1, 2005, 17:43:13  
Job time : 113.108 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 89.7231 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFYGGHGFDPY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	76	100.0	12	3	AAV32225	Aay32225 G-CSF ago
2	52	68.4	121	8	ADP22288	Adp22288 Human ant
3	52	68.4	121	8	ADP22296	Adp22296 Human ant
4	51	67.1	121	8	ADP22284	Adp22284 Human ant
5	46	60.5	331	7	ADE60921	Ade60921 Rat Prote
6	46	60.5	331	8	ADO19157	Ado19157 Human PRO
7	46	60.5	331	8	ADP54207	Adp54207 Human PRO
8	46	60.5	331	8	ADP23166	Adp23166 PRO polyp
9	46	60.5	332	5	ABP69582	Abp69582 Human pol
10	46	60.5	332	7	ADG77005	Adg77005 Human nuc
11	46	60.5	332	7	ADM05821	Adm05821 Human pro
12	46	60.5	332	8	ADI26203	Adi26203 Human pro
13	46	60.5	336	4	ABG18425	Abg18425 Novel hum
14	46	60.5	701	7	ABO81995	Abob81995 Pseudomon
15	45	59.2	121	8	ADP22190	Adp22190 Human ant
16	45	59.2	121	8	ADP22186	Adp22186 Human ant
17	45	59.2	158	8	ADK47356	Adk47356 Streptoco
18	45	59.2	170	8	ADR95130	Adr95130 Novel S.
19	45	59.2	387	4	ABG26063	Abg26063 Novel hum
20	45	59.2	427	4	ABG29887	Abg29887 Novel hum
21	45	59.2	495	4	ABB65066	Abb65066 Drosophil
22	45	59.2	569	7	ABO83544	Abob83544 Pseudomon
23	45	59.2	944	6	ABB80172	Abb80172 A. fumiga
24	44	57.9	47	6	ADA23219	Ada23219 Tropaolu
25	44	57.9	77	6	ADA23218	Ada23218 Tropaolu

26	44	57.9	458	6	ABU22342	Abu22342 Protein e
27	43	56.6	90	5	ABP04474	Abp04474 Human ORF
28	43	56.6	1583	8	ADJ49668	Adj49668 Oil-assoc
29	43	56.6	1724	8	ADJ50155	Adj50155 Oil-assoc
30	43	56.6	1897	4	AAU15088	Aau15088 Protein e
31	43	56.6	1897	5	ABP73203	Abp73203 Candida a
32	42	55.3	905	8	ABM82633	Abm82633 Human dia
33	42	55.3	934	5	ABM82632	Abm82632 Human dia
34	42	55.3	934	8	ABM82631	Abm82631 Human NS
35	42	55.3	935	8	ABM82631	Abm82631 Human dia
36	42	55.3	979	2	AAV06606	Aay06606 Human isl
37	42	55.3	979	4	AAG80205	Aag80205 Human aut
38	42	55.3	979	6	ABU04793	Abu04793 Human exp
39	42	55.3	979	6	ABU04784	Abu04784 Human exp
40	42	55.3	979	6	ABU04789	Abu04789 Human exp
41	42	55.3	979	6	ABU04794	Abu04794 Human exp
42	42	55.3	979	7	ADE57230	Ades7230 Human Pro
43	42	55.3	979	7	ADE56167	Ades6167 Human Pro
44	42	55.3	979	7	ADE57226	Ades7226 Human Pro
45	42	55.3	979	7	ADD45278	Add45278 Human Pro

ALIGNMENTS

RESULT 1	AAV32225	standard; peptide; 12 AA.
XX	AAV32225;	
AC	AAV32225;	
XX		
DT	15-FEB-2000	(first entry)
XX		
DE	G-CSF agonist antibody mAb163-93 heavy chain variable region CDR3.	
XX		
KW	Granulocyte colony stimulating factor receptor; G-CSF; mouse;	
KW	monoclonal antibody; agonist; screening; neutropenia; therapy;	
KW	complementarity determining region; CDR; mAb163-93.	
XX		
OS	Mus musculus.	
XX		
PN	WO9955735-A1.	
XX		
PD	04-NOV-1999.	
XX		
PF	30-APR-1999;	99WO-US009466.
XX		
PR	30-APR-1998;	98US-0083575P.
XX		
PA	(TANO-) TANOX INC.	
PI	Ni B, Sun BNC, Sun CRV;	
XX		
DR	WPI; 2000-052805/04.	
XX		
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic cell lineage progenitors.	
XX		
PS	Claim 13; Page 30; 64pp; English.	
XX		
CC	The present sequence represents complementarity determining region 3 (CDR3) of the heavy chain variable region of murine monoclonal antibody mAb163-93. This antibody is an example of an agonist molecule that specifically binds to or interacts with human granulocyte colony stimulating factor (G-CSF) receptor to stimulate cell proliferation and differentiation, especially by dimerising the receptor or activating phosphorylation of kinases associated with the receptor. Agonist antibodies can be used to stimulate proliferation of G-CSF-dependent cells, e.g. to differentiate leading to a repopulation of neutrophilic granulocyte lineage cells, especially to treat neutropenia (claimed).	
CC	They can also be used to detect human G-CSF receptor immunologically	
XX		
SO	Sequence 12 AA;	

Query Match 100.0%; Score 76; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.7e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGFYGGHPGFDY 12  
|||||  
Db 1 EGFYGGHPGFDY 12

RESULT 2  
ADP22288  
ID ADP22288 standard; protein; 121 AA.

AC ADP22288;

DT 09-SEP-2004 (first entry)

DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:194.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

PN WO2004050683-A2.

XX 17-JUN-2004.

PF 02-DEC-2003; 2003WO-US038281.

PR 02-DEC-2002; 2002US-0430729P.

PA (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;

PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

DR WPI; 2004-480601/45.

DR N-PSDB; ADP22287.

XX

PS Example 10; SEQ ID NO 194; 213pp; English.

XX

CC The present invention describes a human monoclonal antibody (I) that

CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

CC (a) a heavy chain complementarity determining region 1 (CDR1) having the

CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

CC and (b) a light chain CDR1 having the two fully defined 11 amino acid

CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying

CC (M1) the level of TNFa in a patient sample, comprising contacting with

CC (I), and detecting the level of binding between the antibody and TNFa in

CC the sample; (2) a composition comprising the antibody or its functional

CC fragment and a carrier; (3) treating (M2) an animal suffering from a

CC neoplastic, or an immuno-mediated inflammatory disease by selecting an

CC animal in need of treatment for the disease by administering the human

CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced

CC apoptosis in an animal by selecting an animal in need of treatment for

CC TNFa induced apoptosis by administering the human monoclonal antibody of

CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,

CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-

CC disorders, immunomodulator, immunosuppressive, nephrotropic,

CC neuroprotective, vasotropic and antiapoptotic activities, and can be used

CC as a TNFa antagonist. The antibody (I) is useful in the preparation of

CC medicament for treating TNF induced apoptosis, neoplastic disease such as

CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,

CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory

CC diseases such as rheumatoid arthritis, glomerulonephritis,

CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's

CC disease, graft-host reactions, septic shock, cachexia, anorexia, and

CC multiple sclerosis. The present sequence represents a human anti-TNFa

CC antibody heavy chain variable region, which is used in the

CC exemplification of the present invention.

XX

SQ Sequence 121 AA;

Query Match 68.4%; Score 52; DB 8; Length 121;  
Best Local Similarity 75.0%; Pred. No. 2.8;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGFYGGHPGFDY 12  
|||:|  
Db 99 EGDYGYYPFDY 110

RESULT 3  
ADP22296

ID ADP22296 standard; protein; 121 AA.

AC ADP22296;

DT 09-SEP-2004 (first entry)

DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:202.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.

XX

OS Homo sapiens.

PN WO2004050683-A2.

XX 17-JUN-2004.

PF 02-DEC-2003; 2003WO-US038281.

PR 02-DEC-2002; 2002US-0430729P.

PA (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;

PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

DR WPI; 2004-480601/45.

DR N-PSDB; ADP22295.

XX

PT New recombinant human monoclonal antibody that specifically binds to

PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such

PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid



PT arthritis.  
XX  
PS Example 10; SEQ ID NO 202; 213pp; English.  
XX  
XX The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFa in a patient sample, comprising contacting with  
CC (I), and detecting the level of binding between the antibody and TNFa in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNFa induced apoptosis by administering the human monoclonal antibody of  
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis,  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFa  
CC antibody heavy chain variable region, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 121 AA;

Query Match 68.4%; Score 52; DB 8; Length 121;  
Best Local Similarity 75.0%; Pred. No. 2.8;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EGFYGGHPGFDY 12  
|||:|  
Db 99 EGDYGGYPYFDY 110

RESULT 4  
ADP22284  
ID ADP22284 standard; protein; 121 AA.  
XX  
AC ADP22284;

XX  
DT 09-SEP-2004 (first entry)

XX  
DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:190.

KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.

XX  
OS Homo sapiens.

XX  
PN WO2004050683-A2.

XX

PD 17-JUN-2004.

XX  
PF 02-DEC-2003; 2003WO-US038281.

XX  
PR 02-DEC-2002; 2002US-0430729P.

XX  
PA (ABGE-) ABGENIX INC.

XX  
PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
PI Manchulenko K, Faggioli R, Senaldi G, Qiaojuan JS;

XX  
DR WPI, 2004-480601/45.

XX  
DR N-PSDB; ADP22283.

XX  
PT New recombinant human monoclonal antibody that specifically binds to  
PT Tumour Necrosis Factor-alpha, useful for treating neoplastic disease such  
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid

PT arthritis.

XX  
PS Example 10; SEQ ID NO 190; 213pp; English.

XX  
XX The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFa in a patient sample, comprising contacting with  
CC (I), and detecting the level of binding between the antibody and TNFa in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNFa induced apoptosis by administering the human monoclonal antibody of  
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis,  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFa  
CC antibody heavy chain variable region, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 121 AA;

Query Match 67.1%; Score 51; DB 8; Length 121;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EGFYGGHPGFDY 12  
|||:|  
Db 99 EGDYGGNPYFDY 110

RESULT 5  
ADE60921  
ID ADE60921 standard; protein; 331 AA.  
XX  
AC ADE60921;

XX  
DT 29-JAN-2004 (first entry)

XX  
DE Rat Protein NP\_112620, SEQ ID NO 6835.

XX



XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'Urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
DR GENBANK; NP\_112620.  
DR  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 331 AA;

QY 2 GFYGGHPGFDY 12  
|:| | |:  
Db 298 GYGYGPGYDY 308

Query Match 60.5%; Score 46; DB 7; Length 331;  
Best Local Similarity 63.6%; Pred. No. 64;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 6  
ADO19157  
ID ADO19157 standard; protein; 331 AA.  
XX  
AC ADO19157;  
XX

XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human PRO polypeptide #46.  
XX  
XX Human; PRO; immune related disorder; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
KW diabetes mellitus; renal disease; demyelinating disease;  
KW central nervous system; peripheral nervous system;  
KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
KW chronic inflammatory demyelinating polyneuropathy.  
XX  
OS Homo sapiens.  
XX  
PN WO2004043361-A2.  
XX  
PD 27-MAY-2004.  
XX  
PF 06-NOV-2003; 2003WO-US035268.  
XX  
PR 08-NOV-2002; 2002US-0425235P.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
PI Wood WT, Wu TD;  
XX  
XX WPI; 2004-420067/39.  
DR N-PSDB; ADO19156.  
DR  
XX  
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
PT treating an immune related disorder such as systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
PT spondyloarthritis.  
XX  
XX Claim 7; SEQ ID NO 92; 1731pp; English.  
XX  
XX The invention relates to human PRO polypeptides and the polynucleotides  
CC encoding them. The polypeptides and polynucleotides are useful for  
CC treating and diagnosing immune related disorders in mammals. The immune  
CC related disorders include systemic lupus erythematosus, rheumatoid  
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
CC central or peripheral nervous system, demyelinating polyneuropathy,  
CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
CC invention.  
XX  
SQ Sequence 331 AA;

QY 2 GFYGGHPGFDY 12  
|:| | |:  
Db 298 GYGYGPGYDY 308

Query Match 60.5%; Score 46; DB 8; Length 331;  
Best Local Similarity 63.6%; Pred. No. 64;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 7  
ADP54207  
ID ADP54207 standard; protein; 331 AA.  
XX  
AC ADP54207;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human PRO protein sequence SEQ ID NO:183.  
XX

KW	human; PRO; immune related disease; inflammatory immune response;
KW	immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW	antialsthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW	antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW	haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW	nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW	virucide; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO2004039956-A2.
PD	13-MAY-2004.
XX	
PF	28-OCT-2003; 2003WO-US034381.
XX	
PR	29-OCT-2002; 2002US-0422472P.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI	Wood WI, Wu TD;
XX	
DR	WPI; 2004-376182/35.
XX	
DR	N-PSDB; ADP54206.
PT	
PT	New PRO polynucleotides and polypeptides, useful in diagnosing
PT	and treating an immune related disease, e.g. systemic lupus
PT	erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT	stimulating an immune response.
XX	
PS	Claim 1; SEQ ID NO 183; 3009pp; English.
XX	
CC	The present invention describes an isolated PRO nucleic acid (1). Also
CC	described: (1) a vector comprising (1); (2) a host cell comprising the
CC	vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC	isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC	polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC	antibody which specifically binds to a polypeptide of (4); (7) a
CC	composition of matter comprising a polypeptide of (4); an agonist or
CC	antagonist of the polypeptide or an antibody that binds to the
CC	polypeptide in combination with a carrier; (8) an article of manufacture
CC	comprising a container, a label on the container and a composition of
CC	matter of (7); (9) a method of treating an immune related disease in a
CC	mammal; (10) a method for determining the presence of a PRO polypeptide
CC	in a sample suspected of having the polypeptide; (11) a method of
CC	diagnosing an immune related disease or an inflammatory immune response
CC	in mammal; (12) a method of identifying a compound that inhibits or
CC	mimics the activity of or expression of a gene encoding a PRO polypeptide
CC	; and (13) a method of stimulating the immune response in a mammal. The
CC	PRO sequences have antiallergic, antianaemic, antiarthritic,
CC	antirheumatic, antidiabetic, antiinflammatory, gastrointestic,
CC	antirhaumatic, antithyroid, CNS, dermatological, antipsoriatic,
CC	haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC	nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC	virucide activities, and can be used in gene therapy. The nucleic acid
CC	(1) and the encoded polypeptides, compositions, kits and methods are
CC	useful in diagnosing and treating an immune related disease and in
CC	stimulating an immune response. The present sequence represents a human
CC	PRO protein from the present invention.
CC	
XX	
SO	Sequence 331 AA;
	Query Match 60.5%; Score 46; DB 8; Length 331;
	Best Local Similarity 63.6%; Pred. No. 64;
	Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY	2 GFGGHPGFDY 12
	:
DB	298 GYGYGPGYDY 308

ID	ADP23166	standard; protein; 331 AA.
XX	AC	ADP23166;
XX	DT	18-NOV-2004 (first entry)
XX	DE	PRO polypeptide SEQ ID NO:260.
KW	XX	PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
OS	XX	Unidentified.
PN	XX	WO2004041170-A2.
PD	XX	21-MAY-2004.
PF	XX	30-OCT-2003; 2003WO-US034312.
PR	XX	01-NOV-2002; 2002US-0423394P.
PA	XX	(GETH ) GENENTECH INC.
PI	XX	Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PT	XX	Mu TD;
DR	XX	WPI; 2004-419628/39.
N-PSDB;	XX	ADP23165.
PT	XX	New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
Claim 7;	SEQ ID NO 260;	2940pp; English.
The invention relates to a novel isolated nucleic acid and the PRO		
polypeptide encoded by it. A protein of the invention has		
antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,		
osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,		
antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide		
of the invention may have a use in gene therapy. The PRO polypeptide, its		
agonist, antagonist, or antibody that specifically binds to the		
polypeptide is useful for treating an immune related disorder such as		
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,		
jvenile chronic inflammatory myopathy, Sjogren's syndrome, systemic		
vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune		
thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal		
disease, a demyelinating disease of the central or peripheral nervous		
system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,		
a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary		
disease, infectious or autoimmune chronic active hepatitis, primary		
biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,		
inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's		
disease, an autoimmune or immune-mediated skin disease, a bulous skin		
disease, erythema multiforme, contact dermatitis, psoriasis, an allergic		
disease, asthma, allergic rhinitis, atopic dermatitis, food		
hypersensitivity, urticaria, an immunologic disease of the lung,		
eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity		
pneumonitis, a transplantation associated disease, graft rejection or		
graft-versus-host disease. The present sequence represents a PRO protein		
of the invention.		
Sequence 331 AA;		
Query Match	60.5%;	Score 46; DB 8; Length 331;
Best Local Similarity	63.6%;	Pred. No. 64;
Matches 7; Conservative	2; Mismatches	2; Indels 0; Gaps 0;
2 GFYGGHPGFDY	12	

Db 298 GYGYGPGYDY 308

RESULT 9  
ABP69582 ID ABP69582 standard; protein; 332 AA.

XX AC ABP69582;

XX DT 20-JAN-2003 (first entry)

XX DE Human polypeptide SEQ ID NO 1629.

XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic.

XX OS Homo sapiens.

XX PN WO200270539-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US005095.

XX PR 05-MAR-2001; 2001US-00799451.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX DR MPI; 2002-759812/82.

XX DR N-PSDB; AB211799.

PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (ESTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
PT or coagulation disorders.

XX PS Claim 9; SEQ ID NO 1629; 1012pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences (AB211119-  
CC AB212066) or their mature protein coding portion, active domain coding  
CC protein or complementary sequences. The polynucleotides are useful for  
CC identifying expressed genes or for physical mapping of human genome. The  
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
CC markers, as a food supplement, for generating antibodies, in medical  
CC imaging, screening and diagnostic assays and for treating cell-  
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
CC arthritis, etc. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 332 AA;

Query Match 60.5%; Score 46; DB 5; Length 332;  
Best Local Similarity 63.6%; Pred. No. 64;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GFGYGHGPFY 12

Db 299 GYGYGPGYDY 309

RESULT 10  
ADG77005 ID ADG77005 standard; protein; 332 AA.

XX AC ADG77005;

XX DT 11-MAR-2004 (first entry)

XX DE Human nucleic acid associated polypeptide (NAAP) 33.

XX KW nucleic acid associated polypeptide; NAAP; cytostratic;  
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;  
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;  
KW thymimetic; gene therapy; cell proliferative; cancer; atherosclerosis;  
KW neurological; epilepsy; Huntington's disease; stroke; immune;  
KW inflammatory; AIDS; allergy; developmental; Hypothyroidism;  
KW Cushing's syndrome; infection; human.

XX OS Homo sapiens.

XX PN WO2003076586-A2.

XX PD 18-SEP-2003.

XX PF 05-MAR-2003; 2003WO-US007002.

XX PR 06-MAR-2002; 2002US-0362329P.

XX PR 15-MAR-2002; 2002US-0364438P.

XX PR 19-APR-2002; 2002US-0373891P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Richardson TW, Elliott VS, Sprague WW, Jiang X, Tang YT;  
PI Zebadjadian Y, Baughn MR, Jackson AA, Kable AE, Lee EA, Khan FA;  
PI Yue H, Forsythe IJ, Ramkumar J, Griffin JA, Li JX, Marquis JP;  
PI Lehr-Mason PM, Jin P, Hawkins PR, Wilson AD, Swarnakar A, He A;  
PI Hafalia AJA, Tran B, Duggan BM, Emerling BM, Borowsky ML, Yao MG;  
PI Chawla NK, Burford N, Khare R, Lee S, Becha SD, Lee SY;

XX DR MPI; 2003-756814/71.

XX DR N-PSDB; ADG77058.

PT New human nucleic acid associated proteins (NAAP), useful for diagnosing,  
PT treating and preventing diseases or conditions associated with the  
PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or  
PT infections.

XX PS Claim 1; SEQ ID NO 33; 373pp; English.

XX CC This invention relates to a novel isolated human nucleic acid associated  
CC polypeptide (NAAP). The invention may be useful for the development of  
CC compounds with a cytostratic, antiarteriosclerotic, anticonvulsant,  
CC nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,  
CC antiinflammatory or thymimetic activity and also for gene therapy. The  
CC invention may prove useful for the development of treatments for diseases  
CC or conditions associated with the decreased expression or overexpression  
CC of NAAP, such as cell proliferative (for example cancer,  
CC atherosclerosis), neurological (for example epilepsy, Huntington's  
CC disease, stroke), immune/inflammatory (for example AIDS, allergies) and  
CC developmental (for example Hypothyroidism, Cushing's syndrome) disorders,  
CC or infections. The present sequence is that of a human NAAP protein of  
CC the invention.

XX SQ Sequence 332 AA;

Query Match 60.5%; Score 46; DB 7; Length 332;  
Best Local Similarity 63.6%; Pred. No. 64;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



QY 2 GFYGGHPGFDY 12  
Db 299 GYYGYGPGYDY 309

RESULT 11	
ADM05821	
ID	ADM05821 standard; protein; 332 AA.

PT New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.

```

Query Match      60.5%;   Score 46;   DB 7;   Length 332;
Best Local Similarity 63.6%;   Pred. No. 64;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 12	
AD126203	
ID AD126203	standard; protein; 332 AA.

XX human; signal transducer and activator of transcription 6; STAT6;  
 KW immunogen; STAT6 activation; allergy; inflammation; autoimmune disease  
 KW diabetes; hyperlipidaemia; infection; cancer; Th1 hyperactive disease;  
 KW rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus;  
 KW sepsis; asthma; allergic rhinitis; ischaemic heart disease;  
 KW subarachnoid haemorrhage; viral hepatitis; AIDS.

PT	New signal transducer and activator of transcription 6 activation
PT	promoting purified protein, for diagnosing and treating disease
PT	associated with activation/inhibition of transcription factor e.g
PT	diabetes and cancer.

Query Match	60.5%;	Score 46;	DB 8;	Length 332;
Best Local Similarity	63.6%;	Pred. No. 64;		
Matches	7;	Conservative	2;	Mismatches
			2;	Indels
				0;
				Gaps
				0;

RESULT 13  
ABG18425

ID ABG18425 standard; protein; 336 AA.  
XX  
AC ABG18425;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #18416.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS82612.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 48784; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 336 AA;

Query Match 60.5%; Score 46; DB 4; Length 336;  
Best Local Similarity 63.6%; Pred. No. 65;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GFFYGHPGFDY 12  
|:|:|:|:|:|:  
Db 303 GYGYGPGYDY 313

RESULT 14  
ABO81995  
ID ABO81995 standard; protein; 701 AA.  
XX

AC ABO81995;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #14170.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
PE 18-FEB-1999; 99US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
DR WPI; 2003-615309/58.  
DR N-PSDB; ABD15566.  
XX  
XX  
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 30741; 455pp; English.  
XX  
CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 701 AA;

Query Match 60.5%; Score 46; DB 7; Length 701;  
Best Local Similarity 72.7%; Pred. No. 1.4e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 EGFYGHHPGFD 11  
|||:|:|:|:|:  
Db 43 EGLRGHPGCTD 53

RESULT 15  
ADP22190  
ID ADP22190 standard; protein; 121 AA.  
XX  
AC ADP22190;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human anti-TNFA antibody light chain variable region SEQ ID NO:96.  
XX  
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;



KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004050683-A2.  
XX  
PD 17-JUN-2004.  
XX  
PF 02-DEC-2003; 2003WO-US038281.  
XX  
PR 02-DEC-2002; 2002US-0430729P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
PI Haak-Frendscho M, Rathanaawami P, Pigott C, Liang ML, Lee R;  
PI Manchulenchu K, Faggioni R, Senaldi G, Qiaojuan JS;  
XX  
DR WPI; 2004-480601/45.  
DR N-PSDB; ADP22189.  
XX  
PT New recombinant human monoclonal antibody that specifically binds to  
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
PT arthritis.  
XX  
PS Example 10; SEQ ID NO 96; 213pp; English.  
XX  
CC The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFa in a patient sample, comprising contacting with  
CC (I), and detecting the level of binding between the antibody and TNFa in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNFa induced apoptosis by administering the human monoclonal antibody of  
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis,  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNFa  
CC antibody light chain variable region, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 121 AA;

Query Match 59.2%; Score 45; DB 8; Length 121;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGFYGGHPGFDY 12  
Db 99 ESDYGNPYPFDY 110

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Job time : 91.7231 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 23.4462 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFYGHGHPFDY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	60.5	701	4	US-09-252-991A-30741	Sequence 30741, A
2	45	59.2	158	4	US-09-583-110-3871	Sequence 3871, Ap
3	45	59.2	170	4	US-09-107-433-3765	Sequence 3765, Ap
4	45	59.2	569	4	US-09-252-991A-32290	Sequence 32290, A
5	43	56.6	563	4	US-09-248-796A-17268	Sequence 17268, A
6	43	56.6	1897	4	US-09-792-024-98	Sequence 98, Appl
7	42	55.3	979	3	US-08-514-213A-2	Sequence 2, Appli
8	42	55.3	979	4	US-09-015-399-5	Sequence 5, Appli
9	42	55.3	1003	4	US-09-949-016-11260	Sequence 11260, A
10	41	53.9	104	4	US-09-248-796A-24186	Sequence 24186, A
11	41	53.9	341	4	US-09-248-796A-20848	Sequence 20848, A
12	40	52.6	255	4	US-09-248-796A-28030	Sequence 28030, A
13	40	52.6	371	4	US-09-252-991A-18673	Sequence 18673, A
14	40	52.6	819	4	US-09-252-991A-19569	Sequence 19569, A
15	39.5	52.0	243	4	US-09-489-039A-8468	Sequence 8468, Ap
16	39	51.3	26	2	US-08-943-583-5	Sequence 5, Appli
17	39	51.3	26	2	US-08-943-583-6	Sequence 6, Appli
18	39	51.3	27	2	US-08-943-583-1	Sequence 1, Appli
19	39	51.3	168	4	US-09-376-113-5	Sequence 5, Appli
20	39	51.3	175	4	US-09-376-113-7	Sequence 7, Appli
21	39	51.3	176	4	US-09-248-796A-18362	Sequence 18362, A
22	39	51.3	261	4	US-09-248-796A-19618	Sequence 19618, A
23	39	51.3	400	4	US-09-543-681A-4952	Sequence 4952, Ap
24	39	51.3	465	4	US-10-029-180-44	Sequence 44, Appl
25	39	51.3	498	4	US-09-270-767-45042	Sequence 45042, A
26	39	51.3	500	2	US-08-987-519-1	Sequence 1, Appli
27	39	51.3	556	4	US-09-252-991A-18923	Sequence 18923, A

28	38.5	50.7	341	4	US-09-540-236-2889	Sequence 2889, Ap
29	38	50.0	12	3	US-08-836-561-36	Sequence 36, Appl
30	38	50.0	12	4	US-09-434-122-36	Sequence 36, Appl
31	38	50.0	21	4	US-09-010-317-22	Sequence 22, Appl
32	38	50.0	182	4	US-09-513-999C-4828	Sequence 4828, Ap
33	38	50.0	182	4	US-09-513-999C-4831	Sequence 4831, Ap
34	38	50.0	140	3	US-08-836-561-23	Sequence 23, Appl
35	38	50.0	140	4	US-09-434-122-23	Sequence 23, Appl
36	38	50.0	180	4	US-09-248-796A-22820	Sequence 22820, A
37	38	50.0	203	4	US-09-252-991A-26436	Sequence 26436, A
38	38	50.0	223	4	US-09-152-060-116	Sequence 116, App
39	38	50.0	245	4	US-09-533-029-44	Sequence 44, Appl
40	38	50.0	272	4	US-09-949-016-9966	Sequence 9966, Ap
41	38	50.0	272	4	US-09-949-016-9967	Sequence 9967, Ap
42	38	50.0	341	4	US-09-248-796A-18805	Sequence 18805, A
43	38	50.0	362	4	US-09-252-991A-26917	Sequence 26917, A
44	38	50.0	455	4	US-09-538-092-123	Sequence 123, App
45	38	50.0	522	1	US-08-639-237-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-252-991A-30741
; Sequence 30741, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30741
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30741

Query Match      60.5%; Score 46; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 59;
Matches      8; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

QY      1 EGFYGHGHPFD 11
Db      43 EGLRGHPGTD 53

RESULT 2
US-09-583-110-3871
; Sequence 3871, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3871
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LENGTH: 158  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-583-110-3871

Query Match 59.2%; Score 45; DB 4; Length 158;  
Best Local Similarity 77.8%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGFD 11  
| | | | |  
Db 4 FIGHDPFN 12

RESULT 3  
US-09-107-433-3765  
Sequence 3765, Application US/09107433  
Patent No. 6800744

## GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO  
THERAPEUTICS

NUMBER OF SEQUENCES: 5206

## CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

## COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997

## ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

## INFORMATION FOR SEQ ID NO: 3765:

## SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

## FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...170

SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

US-09-107-433-3765

Query Match 59.2%; Score 45; DB 4; Length 170;  
Best Local Similarity 77.8%; Pred. No. 21;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGFD 11  
| | | | |  
Db 16 FIGHDPFN 24

RESULT 4  
US-09-252-991A-32290  
Sequence 32290, Application US/09252991A

Patent No. 6551795

## GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32290

LENGTH: 569

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32290

Query Match 59.2%; Score 45; DB 4; Length 569;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGHPGFD 11  
| | | | |  
Db 45 GGHPGFD 51

RESULT 5  
US-09-248-796A-17268  
Sequence 17268, Application US/09248796A

Patent No. 6747137

## GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17268

LENGTH: 563

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-17268

Query Match 56.6%; Score 43; DB 4; Length 563;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGF 10  
| | | | |  
Db 522 FYGHPGF 529

RESULT 6  
US-09-792-024-98  
Sequence 98, Application US/09792024

Patent No. 6783985

## GENERAL INFORMATION:

APPLICANT: Roemer, Terry

APPLICANT: Jiang, Bo

APPLICANT: Boone, Charles

APPLICANT: Bussey, Howard

```
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/09/792,024
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 1897
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-792-024-98

Query Match          56.6%; Score 43; DB 4; Length 1897;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 EYGGHPPGF 10
      |||||
Db      1294 EYGGHPPGF 1301

RESULT 7
US-08-514-213A-2
; Sequence 2, Application US/08514213A
; Patent No. 6391651
; GENERAL INFORMATION:
; APPLICANT: MacIaren, No. 63916511
; APPLICANT: No. 6391651kins, Abner
; APPLICANT: Ian, Michael
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION AND
; TITLE OF INVENTION: TREATMENT OF INSULIN-DEPENDENT DIABETES
; FILE REFERENCE: 14014.0199
; CURRENT APPLICATION NUMBER: US/08/514,213A
; CURRENT FILING DATE: 1995-08-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. 6391651e =
; US-08-514-213A-2

Query Match          55.3%; Score 42; DB 3; Length 979;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 EGFYGGHPPGF 12
      :|:|:|:|
Db      250 KGIFGDHPGHSY 261

RESULT 8
US-09-015-399-5
; Sequence 5, Application US/09015399
; Patent No. 6770460
; GENERAL INFORMATION:
; APPLICANT: Hinkkanen, Ari
; TITLE OF INVENTION: A New Fusion Protein and Its Use in an
; TITLE OF INVENTION: Immunoassay for the Simultaneous Detection of
; TITLE OF INVENTION: Autoantibodies Related to Insulin-Dependent Diabetes
; TITLE OF INVENTION: Mellitus
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street N.W., Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,399
; FILING DATE: 29-JAN-1998
; CLASSIFICATION: 53f
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-015-399-5

Query Match          55.3%; Score 42; DB 4; Length 979;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 EGFYGGHPPGF 12
      :|:|:|:|
Db      250 KGIFGDHPGHSY 261
```

```
RESULT 9
US-09-949-016-11260
; Sequence 11260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11260
; LENGTH: 1003
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11260

Query Match          55.3%; Score 42; DB 4; Length 1003;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 EGFYGGHPPGF 12
      :|:|:|:|
Db      274 KGIFGDHPGHSY 285

RESULT 10
US-09-248-796A-24186
; Sequence 24186, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
```



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; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24186
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24186

Query Match
Best Local Similarity 53.9%; Score 41; DB 4; Length 104;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGHGPGFD 11
   |||||:
Db 47 GGHGPGFE 53

RESULT 11
US-09-248-796A-20848
; Sequence 20848, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20848
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20848

Query Match
Best Local Similarity 53.9%; Score 41; DB 4; Length 341;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GFYGHGPGFD 11
   |||||:
Db 189 GFYMAHPNYD 198

RESULT 12
US-09-248-796A-28030
; Sequence 28030, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
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```
; SEQ ID NO 28030
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-28030

Query Match
Best Local Similarity 52.6%; Score 40; DB 4; Length 255;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGCHPG 9
   |||||
Db 48 YGCHPG 53

RESULT 13
US-09-252-991A-18673
; Sequence 18673, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18673
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18673

Query Match
Best Local Similarity 52.6%; Score 40; DB 4; Length 371;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GFYGHGPGFD 11
   |||||
Db 87 GAGGHPGFD 96

RESULT 14
US-09-252-991A-19569
; Sequence 19569, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19569
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19569

Query Match
Best Local Similarity 52.6%; Score 40; DB 4; Length 819;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGFYGGHPG 9
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Db 62 QGLVGHPG 70

RESULT 15

US-09-489-039A-8468  
; Sequence 8468, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709,2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 8468  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-8468

Query Match 52.0%; Score 39.5; DB 4; Length 243;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
QY 2 GFYGGHPG-FDY 12  
Db 86 GFVGGKPGAFDF 97

Search completed: March 1, 2005, 17:46:56  
Job time : 24.4462 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 64.2462 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFYGGHPGFDY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	12	14	US-10-071-962-17
2	48	63.2	793	16	US-10-437-963-171397
3	47	61.8	597	15	US-10-425-114-58080
4	46	60.5	332	15	US-10-108-260A-4506
5	45	59.2	944	14	US-10-213-990-27
6	44	57.9	47	14	US-10-178-213-411
7	44	57.9	77	14	US-10-178-213-410
8	44	57.9	458	15	US-10-282-122A-50266
9	43	56.6	122	15	US-10-424-599-277486
10	43	56.6	264	16	US-10-437-963-135092
11	43	56.6	392	16	US-10-437-963-164638
12	43	56.6	1583	15	US-10-389-566-1672
13	43	56.6	1724	15	US-10-389-566-2159

14	43	56.6	1897	14	US-10-032-585-7040	Sequence 7040, Ap
15	42	55.3	176	16	US-10-767-701-39418	Sequence 39418, A
16	42	55.3	184	15	US-10-424-599-177869	Sequence 177869,
17	42	55.3	277	16	US-10-437-963-114358	Sequence 114358,
18	42	55.3	979	14	US-10-038-686-3	Sequence 3, Appli
19	41	53.9	123	15	US-10-424-599-150308	Sequence 150308,
20	41	53.9	146	15	US-10-424-599-181333	Sequence 181333,
21	41	53.9	166	15	US-10-424-599-277458	Sequence 277458,
22	41	53.9	215	15	US-10-425-114-68305	Sequence 68305, A
23	41	53.9	313	9	US-09-928-457-44	Sequence 44, Appl
24	41	53.9	478	15	US-10-425-114-58912	Sequence 58912, A
25	41	53.9	480	15	US-10-425-114-61022	Sequence 61022, A
26	41	53.9	592	14	US-10-032-585-7908	Sequence 7908, Ap
27	40.5	53.3	590	16	US-10-437-963-141380	Sequence 141380,
28	40	52.6	29	14	US-10-340-578-10	Sequence 10, Appl
29	40	52.6	187	14	US-10-180-375-200	Sequence 200, App
30	40	52.6	187	15	US-10-183-687-416	Sequence 416, App
31	40	52.6	187	15	US-10-399-883-34	Sequence 34, Appl
32	40	52.6	190	14	US-10-286-264-14	Sequence 14, Appl
33	40	52.6	190	15	US-10-225-068-134	Sequence 134, App
34	40	52.6	190	15	US-10-374-780A-90	Sequence 90, Appl
35	40	52.6	190	15	US-10-412-699B-306	Sequence 306, App
36	40	52.6	321	16	US-10-437-963-107505	Sequence 107505,
37	40	52.6	491	13	US-10-062-254-272	Sequence 272, App
38	40	52.6	440	15	US-10-424-599-219391	Sequence 219391,
39	40	52.6	455	9	US-09-738-626-6527	Sequence 6527, Ap
40	40	52.6	455	17	US-10-494-541-36	Sequence 36, Appl
41	40	52.6	456	15	US-10-425-114-64327	Sequence 64327, A
42	40	52.6	616	16	US-10-322-281-26	Sequence 26, Appl
43	40	52.6	712	14	US-10-128-714-3108	Sequence 3108, Ap
44	40	52.6	716	14	US-10-128-714-8108	Sequence 8108, Ap
45	39.5	52.0	56	16	US-10-437-963-119540	Sequence 119540,

ALIGNMENTS

RESULT 1  
US-10-071-962-17  
; Sequence 17, Application US/10071962  
; Publication No. US20030170237A1  
; GENERAL INFORMATION:  
; APPLICANT: BauFu Ni  
; APPLICANT: Bill N.C. Sun  
; APPLICANT: Cedily R.Y. Sun  
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
; TITLE OF INVENTION: Screening Method Therefor  
; FILE REFERENCE: 98-3  
; CURRENT APPLICATION NUMBER: US/10/071, 962  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US/09/303, 155A  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/083, 575  
; PRIOR FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-071-962-17

Query Match 100.0%; Score 76; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EGFYGGHPGFDY 12  
Db 1 EGFYGGHPGFDY 12

RESULT 2  
US-10-437-963-171397

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; Sequence 171397, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171397
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_69633C.1.pep
US-10-437-963-171397

Query Match      63.2%; Score 48; DB 16; Length 793;
Best Local Similarity 63.6%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 EGFYGHGPGFD 11
Db      171 DGIYAGHPSPD 181

RESULT 3
US-10-425-114-58080
; Sequence 58080, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58080
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701001844_FLI.pep
US-10-425-114-58080

Query Match      61.8%; Score 47; DB 15; Length 597;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GFYGGHPG 9
Db      122 GFHGGHPG 129

RESULT 4
US-10-108-260A-4506
; Sequence 4506, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4506
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4506

Query Match      60.5%; Score 46; DB 15; Length 332;
Best Local Similarity 63.6%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GFYGGHPGFDY 12
Db      299 GYGYGPGGYDY 309

RESULT 5
US-10-213-990-27
; Sequence 27, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 944
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-27

Query Match      59.2%; Score 45; DB 14; Length 944;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 GFYGGHPGFDY 12
Db      355 GYGYGYTSYDY 365

RESULT 6
US-10-178-213-411
; Sequence 411, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
```



```
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 411
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Tropaeolum majus
US-10-178-213-411
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Query Match      57.9%; Score 44; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EGFYGGH 7
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Db      27 EGFYGGH 33
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## RESULT 7

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US-10-178-213-410
; Sequence 410, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Tropaeolum majus
US-10-178-213-410
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Query Match      57.9%; Score 44; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EGFYGGH 7
         |||||
Db      57 EGFYGGH 63
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## RESULT 8

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US-10-282-122A-50266
; Sequence 50266, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
```

```
; APPLICANT: Forsyth, R.
```

```
; APPLICANT: Xu, H.
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; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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; FILE REFERENCE: ELITRA.034A
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; CURRENT APPLICATION NUMBER: US/10/282,122A
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; CURRENT FILING DATE: 2003-02-20
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; PRIOR APPLICATION NUMBER: 60/191,078
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; PRIOR FILING DATE: 2000-03-21
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; PRIOR APPLICATION NUMBER: 60/206,848
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; PRIOR FILING DATE: 2000-05-23
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; PRIOR APPLICATION NUMBER: 60/207,727
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```
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: 60/230,335
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; PRIOR FILING DATE: 2000-09-06
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; PRIOR APPLICATION NUMBER: 60/230,347
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; PRIOR FILING DATE: 2000-09-09
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; PRIOR APPLICATION NUMBER: 60/242,578
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; PRIOR FILING DATE: 2000-10-23
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; PRIOR APPLICATION NUMBER: 60/253,625
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; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
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; PRIOR APPLICATION NUMBER: 60/267,636
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; PRIOR FILING DATE: 2001-02-09
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; PRIOR APPLICATION NUMBER: 60/269,308
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; Remaining Prior Application data removed - See File Wrapper or PALM.
```

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; NUMBER OF SEQ ID NOS: 78614
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; SOFTWARE: PatentIn version 3.1
```

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; SEQ ID NO 50266
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```
; LENGTH: 458
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```
; TYPE: PRT
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```
; ORGANISM: Burkholderia mallei
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US-10-282-122A-50266
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Query Match      57.9%; Score 44; DB 15; Length 458;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 EGFYGGHPGD 11
         :||| |||
Db      381 QGFYAKHPGD 391
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## RESULT 9

```
US-10-424-599-277486
```

```
; Sequence 277486, Application US/10424599
```

```
; Publication No. US20040031072A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: La Rosa Thomas J
```

```
; APPLICANT: Kovalic David K
```

```
; APPLICANT: Zhou Yihua
```

```
; APPLICANT: Cao Yongwei
```

```
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
```

```
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```
; FILE REFERENCE: 38-21(53223)B
```

```
; CURRENT APPLICATION NUMBER: US/10/424,599
```

```
; CURRENT FILING DATE: 2003-04-28
```

```
; NUMBER OF SEQ ID NOS: 285684
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```
; SEQ ID NO 277486
```

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; LENGTH: 122
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```
; TYPE: PRT
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```
; ORGANISM: Glycine max
```

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; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_92593C.1.pep
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```
US-10-424-599-277486
```

```
Query Match      56.6%; Score 43; DB 15; Length 122;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      3 FYGGHPGD 11
         :||| |||
```

Db 87 YYGHHQGF 95

## RESULT 10

```
US-10-437-963-135092
; Sequence 135092, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135092
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36800C.1.pep
US-10-437-963-135092
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## Query Match

Best Local Similarity 56.6%; Score 43; DB 16; Length 264;  
Best Local Similarity 87.5%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GFGGHPG 9  
|:|||||

Db 171 GYGGHGPG 178

## RESULT 11

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US-10-437-963-164638
; Sequence 164638, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 164638
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_63517C.1.pep
US-10-437-963-164638
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## Query Match

Best Local Similarity 56.6%; Score 43; DB 16; Length 392;  
Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGGHPGFD 11  
|:|||||

Db 360 GYSGHPGND 369

## RESULT 12

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US-10-389-566-1672
; Sequence 1672, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1672
; LENGTH: 1583
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-389-566-1672
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## Query Match

Best Local Similarity 56.6%; Score 43; DB 15; Length 1583;  
Best Local Similarity 87.5%; Pred. No. 6.4e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGF 10  
||:|||||

Db 1158 FYYGHPGF 1165

## RESULT 13

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US-10-389-566-2159
; Sequence 2159, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2159
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-389-566-2159
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## Query Match

Best Local Similarity 56.6%; Score 43; DB 15; Length 1724;  
Best Local Similarity 87.5%; Pred. No. 6.9e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGF 10  
||:|||||

Db 1182 FYYGHPGF 1189

## RESULT 14

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US-10-032-585-7040
; Sequence 7040, Application US/10032585
```

```
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7040
; LENGTH: 1897
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7040
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Query Match      56.6%; Score 43; DB 14; Length 1897;
Best Local Similarity 87.5%; Pred. No. 7.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      3 FYGHPGF 10
      |||||
Db      1294 FYGHPGF 1301
```

```
RESULT 15
US-10-767-701-39418
; Sequence 39418, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39418
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C13495_1.pep
US-10-767-701-39418
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Query Match      55.3%; Score 42; DB 16; Length 176;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EGFYGGHPG 9
      :||:|:|
Db      15 KGFHGGYPG 23
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Search completed: March 1, 2005, 17:52:50
Job time : 65.2462 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 16.2462 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFYGGHPGFY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	49	64.5	378	2	D69793	conserved hypothet
2	46	60.5	137	2	A03865	hypothetical prote
3	46	60.5	353	1	S56750	single stranded D
4	44	57.9	760	2	T16726	hypothetical prote
5	43.5	57.2	174	2	AD2666	conserved hypothet
6	43.5	57.2	192	2	B97448	immunoreactive 14k
7	42	55.3	153	2	AB2666	conserved hypothet
8	42	55.3	153	2	A97448	immunoreactive 14k
9	42	55.3	265	2	G87501	hypothetical prote
10	41	53.9	127	2	E81188	hypothetical prote
11	41	53.9	140	2	S31686	Ig heavy chain V r
12	41	53.9	167	2	AB2796	acetyltransferase
13	41	53.9	167	2	B97575	hypothetical prote
14	41	53.9	223	2	T16654	hypothetical prote
15	41	53.9	308	2	T44427	hypothetical prote
16	41	53.9	322	2	A81990	hypothetical prote
17	41	53.9	917	2	S07183	hypothetical prote
18	41	53.9	1029	2	F87369	TonB-dependent rec
19	41	53.9	1374	2	AE3259	extracellular seri
20	40	52.6	73	2	A60136	keratin, scale (cl
21	40	52.6	78	2	H69905	hypothetical prote
22	40	52.6	127	2	D84469	probable glycine-r
23	40	52.6	390	2	I39570	probable porin [sl
24	40	52.6	486	1	KRXL	keratin 3, type I,
25	40	52.6	641	2	A55549	glucan 1,6-alpha-1
26	40	52.6	732	2	A86395	hypothetical prote
27	40	52.6	739	2	S15727	cellulase (EC 3.2.
28	40	52.6	2059	2	T13858	probable DNA-direc
29	40	52.6	2160	2	T20241	hypothetical prote

30	39.5	52.0	346	2	T49147	nitrilase (EC 3.5.
31	39.5	52.0	346	2	S22398	nitrilase (EC 3.5.
32	39	51.3	135	2	G84469	probable glycine-r
33	39	51.3	148	2	T18236	protein-tyrosine-p
34	39	51.3	176	1	F64725	probable NAD(P)H2
35	39	51.3	176	2	A90635	probable NAD(P)H o
36	39	51.3	176	2	A85486	probable NAD(P)H o
37	39	51.3	184	2	S77928	exoskeletal protei
38	39	51.3	246	2	A84977	hypothetical prote
39	39	51.3	276	2	AD1232	gamma-glutamyl kin
40	39	51.3	276	2	AC1586	gamma-glutamyl kin
41	39	51.3	281	2	E90112	26S proteasome reg
42	39	51.3	306	2	S56259	26S proteasome reg
43	39	51.3	308	2	T43293	multidrug resistan
44	39	51.3	312	2	T33344	hypothetical prote
45	39	51.3	319	2	S44642	hypothetical prote

ALIGNMENTS

RESULT 1  
D69793  
conserved hypothetical protein yeek - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: D69793  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortler  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emmerich, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Faltz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: D69793  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-378 <KUN>  
A;Cross-references: UNIPROT:O31510; GB:Z99107; GB:AL009126; NID:G2632866; PIDN:CAB12505.  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yeek  
Query Match 64.5%; Score 49; DB 2; Length 378;  
Best local Similarity 77.8%; Pred. No. 3.5;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GFYGGHPGF 10  
Db 37 GMYGGHPGY 45  
RESULT 2  
A03865  
hypothetical protein B-137 - human adenovirus 2  
C;Species: Mastadenovirus h2 (human adenovirus 2)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: E92351; E92352; A03865  
R;Gingeras, T.R.; Sciaky, D.; Gelinas, R.E.; Bing-Dong, J.; Yen, C.E.; Kelly, M.M.; Bulic  
J. Biol. Chem. 257, 13475-13491, 1982  
A;Title: Nucleotide sequences from the adenovirus-2 genome.  
A;Reference number: A92351; MUID:83056843; PMID:7142161  
A;Accession: E92351  
A;Molecule type: DNA



A;Residues: 1-137 <GIN>  
A;Cross-references: UNIPROT:P03293  
R;Alestrom, P.; Akusjarvi, G.; Pettersson, M.; Pettersson, U.  
J. Biol. Chem. 257, 13492-13498, 1982  
A;Title: DNA sequence analysis of the region encoding the terminal protein and the hypot  
A;Reference number: A92352; MUID:83056844; PMID:7142162  
A;Accession: E92352  
A;Molecule type: DNA  
A;Residues: 1-137 <ALE>  
C;Superfamily: Mastadenovirus h2 hypothetical protein B-137

Query Match 60.5%; Score 46; DB 2; Length 137;  
Best Local Similarity 54.5%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGFYGHGPF 11  
|:|:|:|:|:|:|:  
Db 75 QGYHGRPGFE 85

RESULT 3  
S56750  
single stranded D box binding factor 2 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: S56750  
R;Smidt, M.P.; Russchen, B.; Snippe, L.; Wijnholds, J.; Ab, G.  
Nucleic Acids Res. 23, 2389-2395, 1995  
A;Title: Cloning and characterisation of a nuclear, site specific ssDNA binding protein.  
A;Reference number: S56750; MUID:95357145; PMID:7630716  
A;Accession: S56750  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-353 <SMI>  
C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology  
F;91-157/Domain: ribonucleoprotein repeat homology <RRM1>  
F;175-241/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 60.5%; Score 46; DB 1; Length 353;  
Best Local Similarity 63.6%; Pred. No. 9.7; Indels 0; Gaps 0;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGYGHGPF 12  
|:|:|:|:|:|:|:  
Db 320 GYGYGPGYDY 330

RESULT 4  
T16726  
hypothetical protein R12B2.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: T16726  
R;Miller, N.  
submitted to the EMBL Data Library, June 1994  
A;Description: The sequence of C. elegans cosmid R12B2.  
A;Reference number: Z18567  
A;Accession: T16726  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-760 <MLI>  
A;Cross-references: EMBL:U00066; NID:g495688; PID:g495693; PIDN:AAA50743.1; CESP:R12B2.5  
A;Experimental source: strain Bristol N2  
C;Genetics:  
A;Gene: CESP:R12B2.5  
A;Introns: 19/2; 94/1; 237/3; 622/3; 728/3

Query Match 57.9%; Score 44; DB 2; Length 760;  
Best Local Similarity 66.7%; Pred. No. 43; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGHPGF 12  
|:|:|:|:|:|:|:

Db 451 YGHPGF 459

RESULT 5  
AD2666  
conserved hypothetical protein Atu0730 [imported] - Agrobacterium tumefaciens (strain C5  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AD2666  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AD2666  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-174 <KUR>  
A;Cross-references: UNIPROT:Q8UHF2; GB:AE008688; PIDN:ALL41746.1; PID:g17739097; GSPDB:G  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: Atu0730  
A;Map position: circular chromosome

Query Match 57.2%; Score 43.5; DB 2; Length 174;  
Best Local Similarity 66.7%; Pred. No. 12; Indels 1; Gaps 1;  
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 GFGYGHGPF-DY 12  
|:|:|:|:|:|:|:  
Db 69 GWYGHGRGYDY 80

RESULT 6  
B97448  
immunoreactive 14K protein bal4k (U62541) [imported] - Agrobacterium tumefaciens (strain  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: B97448  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Accession: B97448  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-192 <KUR>  
A;Cross-references: UNIPROT:Q8UHF2; GB:AE007869; PIDN:AAK86539.1; PID:g15155699; GSPDB:G  
C;Genetics:  
A;Gene: AGR C 1323  
A;Map position: circular chromosome

Query Match 57.2%; Score 43.5; DB 2; Length 192;  
Best Local Similarity 66.7%; Pred. No. 13; Indels 1; Gaps 1;  
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 GFGYGHGPF-DY 12  
|:|:|:|:|:|:|:  
Db 87 GWYGHGRGYDY 98

RESULT 7  
AB2666  
conserved hypothetical protein Atu0728 [imported] - Agrobacterium tumefaciens (strain C5  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AB2666  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AB2666  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-153 <KUR>  
A/Cross-references: UNIPROT:Q8UHF4; GB:AE008688; PIDN:ALL41744.1; PID:g17739095; GSPDB:C  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: Atu0728  
A/Map position: circular chromosome

Query Match 55.3%; Score 42; DB 2; Length 153;  
Best Local Similarity 60.0%; Pred. No. 18;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGFYGGHPGF 10  
:|||||:  
Db 69 DGFYNGHRGY 78

RESULT 8  
A97448  
immunoreactive 14K protein ba14K (U62541) [imported] - Agrobacterium tumefaciens (strain  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: A97448  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: A97448  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-153 <KUR>  
A/Cross-references: UNIPROT:Q8UHF4; GB:AE007869; PIDN:AAK86538.1; PID:g15155698; GSPDB:C  
C/Genetics:  
A/Gene: AGR\_C\_1322  
A/Map position: circular chromosome

Query Match 55.3%; Score 42; DB 2; Length 153;  
Best Local Similarity 60.0%; Pred. No. 18;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGFYGGHPGF 10  
:|||||:  
Db 69 DGFYNGHRGY 78

RESULT 9  
G87501  
hypothetical protein CC2036 [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C/Accession: G87501  
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249; MUID:21173698; PMID:11259647  
A/Accession: G87501  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-265 <STO>  
A/Cross-references: UNIPROT:Q9A6P8; GB:AE005673; NID:g13423511; PIDN:AAK24011.1; GSPDB:C  
C/Genetics:  
A/Gene: CC2036

Query Match 55.3%; Score 42; DB 2; Length 265;  
Best Local Similarity 77.8%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 FYGGHPGFD 11  
:|||||:  
Db 73 FYAGHYGFD 81

RESULT 10  
E81188  
hypothetical protein NMB0515 [imported] - Neisseria meningitidis (strain MC58 serogroup  
C/Species: Neisseria meningitidis  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: E81188  
R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizze, M.  
Science 287, 1809-1815, 2000  
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve  
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A/Reference number: A81000; MUID:20175755; PMID:10710307  
A/Accession: E81188  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-127 <TET>  
A/Cross-references: UNIPROT:Q9K0R5; GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF4094  
A/Experimental source: serogroup B, strain MC58  
C/Genetics:  
A/Gene: NMB0515  
C/Superfamily: Neisseria meningitidis hypothetical protein NMB0515

Query Match 53.9%; Score 41; DB 2; Length 127;  
Best Local Similarity 63.6%; Pred. No. 21;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGFDY 12  
:|||||:  
Db 21 GRYGGNNGFDH 31

RESULT 11  
S31686  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31686  
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31686  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140 <CU1>  
A/Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 53.9%; Score 41; DB 2; Length 140;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 FYGGHPGFDY 12  
:|||||:  
Db 120 FAGGSPSPDY 129

RESULT 12  
AB2796  
acetyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revistion 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AB2796  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AB2796  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-167 <KUR>  
A;Cross-references: UNIPROT:Q8UEH2; GB:AE008688; PIDN:AAL42784.1; PID:g17740228; GSPDB:C  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: Atu1785  
A;Map position: circular chromosome

Query Match 53.9%; Score 41; DB 2; Length 167;  
Best Local Similarity 70.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GFYGGHPGFD 11  
| | | | |  
Db 154 GIVGFHPGFD 163

RESULT 13  
B97575  
hypothetical protein AGR\_C\_3283 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revistion 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: B97575  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Accession: B97575  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-167 <KUR>  
A;Cross-references: UNIPROT:Q8UEH2; GB:AE007869; PIDN:AAK87555.1; PID:g15156891; GSPDB:C  
C;Genetics:  
A;Gene: AGR\_C\_3283  
A;Map position: circular chromosome

Query Match 53.9%; Score 41; DB 2; Length 167;  
Best Local Similarity 70.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GFYGGHPGFD 11  
| | | | |  
Db 154 GIVGFHPGFD 163

RESULT 14  
T16654  
hypothetical protein R02F2.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revistion 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T16654  
R;Pauley, A.  
submitted to the EMBL Data Library, May 1994  
A;Description: The sequence of C. elegans cosmid R02F2.  
A;Reference number: Z18555  
A;Accession: T16654  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-223 <PAU>

A;Cross-references: UNIPROT:Q21648; EMBL:U00055; NID:g485143; PID:g485148; PIDN:AAA50721.  
A;Experimental source: strain Bristol N2  
C;Genetics:  
A;Gene: CESP:R02F2.5  
A;Introns: 22/3; 38/3

Query Match 53.9%; Score 41; DB 2; Length 223;  
Best Local Similarity 61.5%; Pred. No. 37;  
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 GFYG--GHPGFDY 12  
| | | | | : | | | | :  
Db 198 GFYGGYGGGFD 210

RESULT 15  
T44427  
hypothetical protein - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 21-Jan-2000 #sequence\_revistion 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T44427  
R;Shimanuki, M.; Saka, Y.; Yanagida, M.; Toda, T.  
J. Cell Sci. 108, 569-579, 1995  
A;Title: A novel essential fission yeast gene pad1+ positively regulates pap1+-dependent  
A;Reference number: 222764; MUID:95286704; PMID:7769002  
A;Accession: T44427  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-308 <SHI>  
A;Cross-references: UNIPROT:P41878; EMBL:D31731; NID:g497632; PIDN:BAA06529.1; PID:g4976;  
C;Genetics:  
A;Gene: pad1+

Query Match 53.9%; Score 41; DB 2; Length 308;  
Best Local Similarity 66.7%; Pred. No. 51;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGF 10  
| : | | | | |  
Db 109 GWYNHHPGF 117

Search completed: March 1, 2005, 17:44:45  
Job time : 17.2462 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 77.7231 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFYGHGHPFDY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	65.8	340	2 Q6NYU8	Q6nyu8 brachydanio
2	50	65.8	340	2 Q7ZUJ9	Q7zuJ9 brachydanio
3	49	64.5	63	2 Q655W7	Q655W7 oryza sativ
4	49	64.5	145	2 Q31510	O31510 bacillus su
5	48	63.2	793	2 Q7XPR9	Q7xpr9 oryza sativ
6	46	60.5	117	2 Q8CIR3	Q8cir3 mus musculu
7	46	60.5	137	1 Y137_ADE02	P03293 human adeno
8	46	60.5	196	2 Q7VWWS	Q7vwws bordetella
9	46	60.5	196	2 Q7W9K1	Q7w9k1 bordetella
10	46	60.5	311	2 Q80XR6	Q80xr6 mus musculu
11	46	60.5	324	2 Q7ZYE9	Q7zye9 xenopus lae
12	46	60.5	326	2 Q6GM69	Q6gm69 xenopus lae
13	46	60.5	331	1 ROAA_HUMAN	Q99729 homo sapien
14	46	60.5	331	2 O883I1	O883i1 rattus norv
15	46	60.5	332	2 Q9QX81	Q9qx81 rattus norv
16	46	60.5	506	2 Q6QA65	Q6qa65 rhipicephal
17	45	59.2	184	2 Q7Q1T9	Q7q1t9 anopheles g
18	45	59.2	297	2 Q8E4S3	Q8e4s3 streptococc
19	45	59.2	316	2 Q8KLB5	Q8klb5 rhizobium e
20	45	59.2	316	2 Q93JR7	Q93jr7 rhizobium e
21	45	59.2	495	2 Q9VHX1	Q9vnx1 drosophila
22	44	57.9	143	2 Q7QA33	Q7qa33 anopheles g
23	44	57.9	441	2 Q6ZGB2	Q6zgb2 burkholderi
24	44	57.9	441	2 Q63Q59	Q63q59 burkholderi
25	44	57.9	485	2 Q804G3	Q804g3 brachydanio
26	44	57.9	777	2 Q8MPZ3	Q8mpz3 caenorhabdi
27	44	57.9	780	1 YNL5_CAEEL	Q21955 caenorhabdi
28	44	57.9	1645	2 Q7Q6K9	Q7q6k9 anopheles g
29	43.5	57.2	174	2 Q8UHF2	Q8uhf2 agrobacteri
30	43.5	57.2	192	2 Q7DOT7	Q7dot7 agrobacteri
31	43.5	57.2	1624	2 Q7PT13	Q7pt13 anopheles g

32	43	56.6	155	2 Q92P15	Q92p15 rhizobium m
33	43	56.6	157	2 Q6CVV2	Q6cvv2 kluyveromyc
34	43	56.6	182	2 Q8J0A6	Q8j0a6 cryptococcu
35	43	56.6	182	2 Q8J0C6	Q8j0c6 cryptococcu
36	43	56.6	212	2 Q949F9	Q949f9 oryza sativ
37	43	56.6	214	2 Q6H3Y0	Q6h3y0 oryza sativ
38	43	56.6	392	2 Q8RZF8	Q8rzf8 oryza sativ
39	43	56.6	420	2 Q8U4C7	Q8u4c7 pyrococcus
40	43	56.6	455	2 Q7VID8	Q7vid8 helicobacte
41	43	56.6	497	2 Q6NRR0	Q6nr0 xenopus lae
42	43	56.6	979	1 PTPN_BOVIN	P56722 bos taurus
43	43	56.6	1583	2 Q8J2S9	Q8j2s9 cryptococcu
44	43	56.6	1689	2 Q7Q532	Q7q532 anopheles g
45	43	56.6	1724	2 Q93927	Q93927 cryptococcu

ALIGNMENTS

RESULT 1  
Q6NYU8 PRELIMINARY; PRT; 340 AA.  
AC Q6NYU8; 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Heterogeneous nuclear ribonucleoprotein A/B.  
GN Name=hnrpab;  
OS Brachydanio rerio (Zeprafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquelland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.B., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strausberg R.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC066454; AA166454.1; .  
DR ZFIN; ZDB-GENE-030131-185; hnrpab.  
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.  
DR GO; GO:0019013; C:vital nucleocapsid; IEA.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS50102; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
KW Nucleocapsid; Ribonucleoprotein.  
SQ SEQUENCE 340 AA; 37110 MW; 75C4F9E7C5B60913 CRC64;







```
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wamburt R., Wedler E., Wedler H.,
RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
DR EMBL; 299107; CAB12505.2; -.
DR PIR; D69793; D69793.
KW Complete proteome.
SQ SEQUENCE 145 AA; 15916 MW; 19252CB3E95EAB17 CRC64;

Query Match
Best Local Similarity 64.5%; Score 49; DB 2; Length 145;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GFGYGHPGF 10
Db 37 GMYGHPGY 45

RESULT 5
Q7XPR9 PRELIMINARY; PRT; 793 AA.
ID Q7XPR9;
AC Q7XPR9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0065017.12 protein.
GN Name=OSJNBa0065017.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.,
RT "Sequence and analysis of rice chromosome 4."
RL Nature 420:316-320(2002).
DR EMBL; AL606682; CAB03487.2; -.
DR HSSP; Q99405; 1MPT.
DR Gramene; Q7XPR9; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003137; PA.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR009020; Prot_inh_propept.
DR InterPro; IPR010259; Prot_inh_S8A.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF05922; Subtilisin_N; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
SQ SEQUENCE 793 AA; 83568 MW; 920B578B2A4700C0 CRC64;

Query Match
Best Local Similarity 63.2%; Score 48; DB 2; Length 793;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 BGFYGHHPGFD 11
Db 171 DGIYAGHPSFD 181

RESULT 6
Q8CIR3 PRELIMINARY; PRT; 117 AA.
ID Q8CIR3
AC Q8CIR3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CARG-binding factor A (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22201804; PubMed=12086581;
RA Dean J.L., Sully G., Wait R., Rawlinson L., Clark A.R., Saklatvala J.,
RT "Identification of a novel AU-rich-element-binding protein which is
RT related to AUF1."
RL Biochem. J. 366:709-719(2002).
DR EMBL; AY137376; AAN39116.1; -.
FT NON TER 1
SQ SEQUENCE 117 AA; 13081 MW; 0B90B96695732A60 CRC64;

Query Match
Best Local Similarity 60.5%; Score 46; DB 2; Length 117;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGYGHHPGFDY 12
Db 84 GYGYGPGYDY 94

RESULT 7
Y137_ADE02 STANDARD; PRT; 137 AA.
ID Y137_ADE02
AC P03293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Hypothetical protein B-137.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83056843; PubMed=7142161;
RA Gingeras T.R., Sciaky D., Gelinas R.E., Bing-Dong J., Yen C.E.,
RA Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.,
RT "Nucleotide sequences from the adenovirus-2 genome."
RL J. Biol. Chem. 257:13475-13491(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83056844; PubMed=7142162;
RA Alestroem P., Akusjallvi G., Pettersson M., Pettersson U.,
RT "DNA sequence analysis of the region encoding the terminal protein and
RT the hypothetical N-gene product of adenovirus type 2."
RL J. Biol. Chem. 257:13492-13498(1982).
RN [3]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
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DR EMBL; J01917; -; NOT\_ANNOTATED\_CDS.

DR PIR; E92351; A03865.

KM Hypothetical protein.

SQ SEQUENCE 137 AA; 14356 MW; B7ACA61A63116856 CRC64;

Query Match

Best Local Similarity 60.5%; Score 46; DB 1; Length 137;  
Matches 6; Conservative 54.5%; Pred. No. 13; Mismatches 4; Indels 1; Gaps 0;

Qy 1 EGFYGHGPGFD 11

Db 75 QGYHGRPGCFE 85

RESULT 8

Q7VWWS

ID Q7VWWS PRELIMINARY; PRT; 196 AA.

AC Q7VWWS; 25, Created

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Putative lipoprotein.

GN OrderedLocustNames=BP2072;

OS Bordetella pertussis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Alcaligenaceae; Bordetella.

OX NCBI\_TaxID=520;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Feltham T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagers K.,

RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT Bordetella parapertussis and Bordetella bronchiseptica.";

RL Nat. Genet. 35:32-40(2003).

DR EMBL; BX640417; CAE42350.1; -

KM Complete proteome; Lipoprotein.

SQ SEQUENCE 196 AA; 21519 MW; FF6E2E86B5EE968 CRC64;

Query Match

Best Local Similarity 60.5%; Score 46; DB 2; Length 196;  
Matches 7; Conservative 63.6%; Pred. No. 19; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GFYGHGPGFDY 12

Db 114 GFYGWPYGYW 124

RESULT 9

Q7W9K1

ID Q7W9K1 PRELIMINARY; PRT; 196 AA.

AC Q7W9K1; 25, Created

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Putative lipoprotein.

GN OrderedLocustNames=BP1756;

OS Bordetella parapertussis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Alcaligenaceae; Bordetella.

OX NCBI\_TaxID=519;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=12822 / ATCC BAA-587;

RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Feltham T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagers K.,

RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT Bordetella parapertussis and Bordetella bronchiseptica.";

RL Nat. Genet. 35:32-40(2003).

DR EMBL; BX640428; CAE37057.1; -

KM Complete proteome; Lipoprotein.

SQ SEQUENCE 196 AA; 21562 MW; D082FBA6A6C3A765 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 196;

Best Local Similarity 63.6%; Pred. No. 19;

Matches 7; Conservative 62; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GFYGHGPGFDY 12

Db 114 GFYGWPYGYW 124

RESULT 10

Q80XR6

ID Q80XR6 PRELIMINARY; PRT; 311 AA.

AC Q80XR6; 24, Created

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Hnrapab protein.

GN Name=Hnrapab;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulian S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC043069; AAH43069.1; -

DR HSSP; Q14103; 1HD1.

DR MGI; MGI:1330294; Hnrapab.

DR InterPro; IPR000504; RNA\_rec\_mot.

DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
SQ SEQUENCE 311 AA; 33816 MW; BC23A2C44B9E3025 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 311;  
Best Local Similarity 63.6%; Pred. No. 31;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGGHPGFDY 12  
Db 299 GYGYGPGYDY 309

## RESULT 11

ID Q7ZY9 PRELIMINARY; PRT; 324 AA.  
AC Q7ZY9;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hnnpab-prov protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC043814; AAH43814.1; -.  
DR HSSP; Q14103; 1HD1.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS50102; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
SQ SEQUENCE 324 AA; 35785 MW; BBB84I3ACD2F6456 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 324;  
Best Local Similarity 63.6%; Pred. No. 32;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGGHPGFDY 12  
Db 291 GYGYGPGYDY 301

## RESULT 12

ID Q6GM69 PRELIMINARY; PRT; 326 AA.  
AC Q6GM69;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Klein S., Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC074212; AAH74212.1; -.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS50102; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 326 AA; 35938 MW; F6517A4610F31F2C CRC64;

Query Match 60.5%; Score 46; DB 2; Length 326;  
Best Local Similarity 63.6%; Pred. No. 32;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



QY 2 GFYGHGPFDDY 12  
|:|:|:|:|:|  
Db 293 GYGYGPGYDY 303

RESULT 13  
ROAA\_HUMAN STANDARD; PRT; 331 AA.  
AC Q99729; Q04150; Q8N7U3; Q9BQ99;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC-1 binding protein 1) (ABBP-1).  
GN Name=HNRPA; Synonyms=ABBP1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OC NCBI\_TaxID=9606;  
CX [1]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RX MEDLINE=92008653; PubMed=1717314; DOI=10.1016/0014-5793(91)81249-8;  
RA Khan F., Jalwal A.K., Szer W.;  
RT "Cloning and sequence analysis of a human type A/B hnRNP protein.";  
RL FEBS Lett. 290:159-161 (1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Placenta;  
RX MEDLINE=97153092; PubMed=8999813; DOI=10.1074/jbc.272.3.1452;  
RA Lau P.P., Zhu H.J., Nakamura M., Chan L.;  
RT "Cloning of an APOBEC-1-binding protein that also interacts with apolipoprotein B mRNA and evidence for its involvement in RNA editing".  
RT J. Biol. Chem. 272:1452-1455 (1997).  
RL [3]  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Testis;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Mubashiro K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Shigano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Mizushima K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human cDNAs.";  
RL Nat. Genet. 36:40-45 (2004).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, Skin, and Uterus;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mulhaly S.J.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Binds single-stranded RNA. Has a high affinity for G-rich and U-rich regions of hnRNA. Also binds to APOB mRNA transcripts around the RNA editing site.  
CC -!- SUBUNIT: Interacts with APOBEC1.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q99729-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q99729-2; Sequence=VSP\_007826, VSP\_007827, VSP\_007828;  
CC Name=3;  
CC IsoId=Q99729-3; Sequence=VSP\_007826, VSP\_007827, VSP\_007828, VSP\_007829;  
CC Name=4;  
CC IsoId=Q99729-4; Sequence=VSP\_007829;  
CC -!- TISSUE SPECIFICITY: Ubiquitous.  
CC -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M65028; AAA36575.1; -;  
CC EMBL; U76713; AAC50956.1; -;  
CC EMBL; AK097657; BAC05134.1; -;  
CC EMBL; BC001616; AAH01616.1; -;  
CC EMBL; BC002625; AAH02625.1; -;  
CC EMBL; BC004561; AAH04561.1; -;  
CC EMBL; BC009359; AAH09359.1; -;  
CC EMBL; BC036708; AAH36708.1; -;  
CC PIR; S17563; S17563.  
CC HSSP; Q14103; LIQT.  
CC SWISS-2DPAGE; Q99729; HUMAN.  
CC Genew; HGNC:5034; HNRPA.  
CC MIM; 602688; -;  
CC InterPro; IPR00504; RNA\_rec\_mot.  
CC Pfam; PF00076; RRM\_1; 2.  
CC PROSITE; PS50102; RRM; 2.  
CC Alternative splicing: Nuclear protein; Repeat; RNA-binding.  
CC DOMAIN 68 153 RNA-binding (RRM) 1.  
CC DOMAIN 152 232 RNA-binding (RRM) 2.  
CC DOMAIN 240 323 Gly-rich.  
CC VARSPPLIC 26 32 ASRRGW -> GESPAAG (in isoform 2 and isoform 3).  
CC FT /FTId=VSP\_007826.  
CC FT LEAPRRPRAGIRTA PR -> AGGATAAPPSGNQNGAEG  
CC FT (in isoform 2 and isoform 3).  
FT

FT VARSPLIC 163 164 /FTid=VSP\_007827.  
FT VARSPLIC 264 310 /FTid=VSP\_007828.  
FT VARSPLIC 264 310 Missing (in isoform 3 and isoform 4).  
SQ SEQUENCE 331 AA; 36613 MW; E49C2FD9CF220ADC CRC64;

Query Match  
Best Local Similarity 60.5%; Score 46; DB 1; Length 331;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGFDY 12  
DB 298 GYGYGPGYDY 308

RESULT 14  
088311 PRELIMINARY; PRT; 331 AA.

ID 088311  
AC 088311;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE ALF-C1.  
GN Name=alf-cl;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21142401; PubMed=11245986; DOI=10.1016/S0378-1119(00)00592-8;  
RA Yabuki T., Miyagi S., Ueda H., Saitoh Y., Tsutsumi K.;  
RT "A novel growth-related nuclear protein binds and inhibits rat  
RL aldolase B gene promoter.";  
RL Gene 264:123-129(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Ito K.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB016536; BAA32032.1; -.  
DR PIR; PC4375; PC4375.  
DR PIR; PC4376; PC4376.  
DR PIR; PC4377; PC4377.  
DR HSSP; Q14103; 1HD1.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
SQ SEQUENCE 331 AA; 36206 MW; 89F3B63FC5955A54 CRC64;

Query Match  
Best Local Similarity 60.5%; Score 46; DB 2; Length 331;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGFDY 12  
DB 298 GYGYGPGYDY 308

RESULT 15

Q9QX81 PRELIMINARY; PRT; 332 AA.  
AC Q9QX81;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Type A/B hnRNP p40 (Heterogeneous nuclear ribonucleoprotein).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Leverrier S., Cinato E., Paul C., Derancourt J., Bemark M.,  
RA Leanderson T., Legraverend C.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ238854; CAB62553.1; -.  
DR PIR; PC4375; PC4375.  
DR PIR; PC4376; PC4376.  
DR PIR; PC4377; PC4377.  
DR HSSP; Q14103; 1HD1.  
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.  
DR GO; GO:0019013; C:viral nucleocapsid; IEA.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
KW Nucleocapsid; Ribonucleoprotein.  
SQ SEQUENCE 332 AA; 36233 MW; 414CE08E42A5F921 CRC64;

Query Match  
Best Local Similarity 60.5%; Score 46; DB 2; Length 332;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGFDY 12  
DB 299 GYGYGPGYDY 309

Search completed: March 1, 2005, 17:43:15  
Job time : 79.7231 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 119.631 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRTRKNYL 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*

2: geneseqp19908:\*

3: geneseqp20008:\*

4: geneseqp20018:\*

5: geneseqp20028:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	100.0	17	3	AAY32226	Aay32226 G-CSF ago
2	72	96.0	17	2	AAR76082	Aar76082 Mab 55.1
3	72	96.0	218	7	ADD05274	Add05274 Female mo
4	72	96.0	218	8	ADM80365	Adm80365 Murine ho
5	72	96.0	219	2	AAR76086	Aar76086 Mab 55.1
6	72	96.0	239	2	AAR76087	Aar76087 Mab 55.1
7	72	96.0	244	8	ADR59117	Adr59117 Anti-K88/
8	72	96.0	288	2	AAW82743	Aaw82743 Fusion pr
9	72	96.0	673	2	AAW82742	Aaw82742 plasmid p
10	68	90.7	17	3	AAB07951	Aab07951 CDR1 sequ
11	68	90.7	110	2	AAW56520	Aaw56520 Anti-DNA
12	68	90.7	111	6	ABR42303	AbR42303 Mouse mon
13	68	90.7	111	6	ABR42302	AbR42302 Mouse mon
14	68	90.7	113	7	ADC03128	Adc03128 Colon spe
15	68	90.7	115	8	ADO32150	Ado32150 Colon spe
16	68	90.7	132	3	AAB07964	Aab07964 Amino aci
17	68	90.7	132	3	AAB07966	Aab07966 A light c
18	68	90.7	219	2	AAAR4495	Aaar4495 Sequence
19	68	90.7	246	8	ADQ27057	Adq27057 Human ant
20	68	90.7	247	7	ADC03132	Adc03132 Colon spe
21	68	90.7	249	2	AAW60770	Aaw60770 Single ch
22	68	90.7	267	6	ABR42292	AbR42292 Bispecifi
23	68	90.7	267	6	ABR42299	AbR42299 Bispecifi
24	68	90.7	267	6	ABR42296	AbR42296 Bispecifi
25	68	90.7	267	6	ABR42294	AbR42294 Bispecifi

26	68	90.7	268	6	ABR42288	AbR42288 Diabody 6
27	68	90.7	268	6	ABR42287	AbR42287 Diabody 6
28	68	90.7	268	6	ABR42286	AbR42286 Diabody 6
29	68	90.7	268	6	ABR42297	AbR42297 Diabody h
30	68	90.7	268	6	ABR83644	AbR83644 h679-scfv
31	68	90.7	268	6	ABR83643	AbR83643 679-scfv-
32	68	90.7	391	6	ABR83649	AbR83649 TS1 VL ch
33	65	86.7	17	2	AAW70908	Aaw70908 CDR1 of t
34	65	86.7	100	2	AAW70948	Aaw70948 Light cha
35	65	86.7	265	2	AAR52864	Aar52864 Glycophor
36	64	85.3	208	7	ADD05282	Add05282 Female mo
37	63	84.0	17	7	ADD94188	Add94188 Mouse HUI
38	63	84.0	116	3	AAB15673	Ab15673 Murine 5B
39	60	80.0	113	2	AAAY50145	Aay50145 Antibody
40	60	80.0	113	2	AAAY50143	Aay50143 Antibody
41	60	80.0	113	2	AAAY50144	Aay50144 Antibody
42	60	80.0	113	2	AAAY21818	Aay21818 11E10 ant
43	60	80.0	113	6	ABB98748	Abb98748 Human res
44	60	80.0	113	6	ABB98749	Abb98749 Human res
45	60	80.0	113	6	ABB98747	Abb98747 Human res

ALIGNMENTS

RESULT 1	AAAY32226	standard; peptide; 17 AA.
ID	AAAY32226	
AC	AAAY32226;	
XX		
DT	15-FEB-2000	(first entry)
XX		
DE	G-CSF agonist antibody mAb163-93 light chain variable region CDR1.	
XX		
KW	Granulocyte colony stimulating factor receptor; G-CSF; mouse;	
KW	monoclonal antibody; agonist; screening; neutropenia; therapy;	
KW	complementarity determining region; CDR; mAb163-93.	
XX		
OS	Mus musculus.	
XX		
PN	WO9955735-A1.	
XX		
PD	04-NOV-1999.	
XX		
PF	30-APR-1999;	99WO-US009466.
XX		
PR	30-APR-1998;	98US-0083575P.
XX		
PA	(TANO-) TANOX INC.	
XX		
PI	Ni B, Sun BNC, Sun CRY;	
XX		
DR	WPI; 2000-052805/04.	
XX		
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic cell lineage progenitors.	
XX		
PS	Claim 13; Page 30; 64pp; English.	
XX		
CC	The present sequence represents complementarity determining region 1 (CDR1) of the light chain variable region of murine monoclonal antibody mAb163-93. This antibody is an example of an agonist molecule that specifically binds to or interacts with human granulocyte colony stimulating factor (G-CSF) receptor to stimulate cell proliferation and differentiation, especially by dimerising the receptor or activating phosphorylation of kinases associated with the receptor. Agonist antibodies can be used to stimulate proliferation of G-CSF-dependent cells, e.g. to differentiate leading to a repopulation of neutrophilic granulocyte lineage cells, especially to treat neutropenia (claimed). They can also be used to detect human G-CSF receptor immunologically	
XX		
SQ	Sequence 17 AA;	

Query Match 100.0%; Score 75; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| | | | | | | | | | | | | | | | | |  
Db 1 KSSQSLSSRTRKNYL 16

RESULT 2  
AAR76082  
ID AAR76082 standard; peptide; 17 AA.

AC AAR76082;  
XX  
XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX  
DE Mab 55.1 light chain CDR1.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.

OS Mus sp.  
XX  
XX WO9515382-A1.  
XX  
XX 08-JUN-1995.  
XX  
XX 29-NOV-1994; 94WO-GB002610.  
XX  
XX 03-DEC-1993; 93GB-00024819.  
PR 03-JUN-1994; 94GB-00011089.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX PA  
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;  
XX  
XX WPI; 1995-215262/28.

PT Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.

PS Claim 2; Page 97; 121pp; English.

XX  
XX An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
CC of the heavy and light chains of Mab 55.1 (ECACC 93081901), which  
CC recognises the colorectal tumor-associated antigen CA55.1. It is  
CC optionally humanized and in the form F(ab')<sub>2</sub>, F(ab)'<sub>2</sub>, Fab, Fv, scFv or V-  
CC min, and is produced in transgenic animals or plants. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX

SQ Sequence 17 AA;

Query Match 96.0%; Score 72; DB 2; Length 17;  
Best Local Similarity 93.8%; Pred. No. 8.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| | | | | | | | | | | | | | | | | |  
Db 1 KSSQSLSSRTRKNYL 16

RESULT 3  
ADD05274  
ID ADD05274 standard; protein; 218 AA.

AC ADD05274;  
XX  
XX 01-JAN-2004 (first entry)  
XX  
DE Female mouse sex hormone of the invention #6.  
XX  
KW female sex hormone.  
XX  
OS Mus sp.

XX  
XX WO2003074704-A1.  
XX  
XX 12-SEP-2003.  
PD  
XX  
XX 28-FEB-2003; 2003WO-JP002311.  
PF  
XX  
XX 01-MAR-2002; 2002JP-00055669.  
PR  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Katagiri M, Fujimoto S, Goda Y;  
XX  
XX WPI; 2003-731681/69.  
DR  
XX  
XX N-PSDB; ADD05273.  
DR  
XX  
XX Novel proteins for binding, identifying and concentrating female sex  
PT hormones.  
PT  
XX  
XX Claim 1; SEQ ID NO 12; 101pp; Japanese.

XX  
XX The present invention relates to proteins that bind to female sex  
CC hormones. The method is useful for binding, identifying and concentrating  
CC female sex hormones. The present invention represents a female sex  
CC hormone of the invention.  
XX

SQ Sequence 218 AA;

Query Match 96.0%; Score 72; DB 7; Length 218;  
Best Local Similarity 93.8%; Pred. No. 0.00016;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| | | | | | | | | | | | | | | | | |  
Db 24 KSSQSLSSRTRKNYL 39

RESULT 4  
ADM80365  
ID ADM80365 standard; protein; 218 AA.

XX  
XX ADM80365;  
XX  
XX 03-JUN-2004 (first entry)  
DT

XX  
DE Murine hormone disruptor EE2-3 antibody (scFv) protein SeqID 12.  
XX  
KW antibody; mouse; murine; scFv; hormone disruptor; alkylphenol;  
KW resin component; chlorophenol; immunological isolation;  
KW environmental protection.  
KW  
XX

OS Mus sp.

XX  
XX WO2003101611-A1.

XX  
XX 11-DEC-2003.

XX  
XX 30-MAY-2003; 2003WO-JP006840.

XX  
XX 31-MAY-2002; 2002JP-00159728.

XX  
XX (NIEN-) JAPAN ENVIROCHEMICALS LTD.  
PA (ENVI-) ENVIRONMENT PURIFICATION RES INST INC.  
XX

PI Saito K, Shiraishi T, Goda Y;  
XX WPI; 2004-043011/04.  
DR N-PSDB; ADM80364.  
XX  
PT Polymer-molded support carrying anti-hormone-disrupting-substance  
PT antibody for immunological isolation, concentration or clean-up of such  
PT trace hormone disruptors in samples, applicable in environmental  
PT protection.  
XX  
PS Example 7; SEQ ID NO 12; 133pp; Japanese.  
XX  
CC This invention relates to a novel material useful for the isolation of  
CC hormone disrupting substances (i.e. hormone disruptors). Specifically, it  
CC refers to a material that comprises a polymer-molded support carrying an  
CC anti-hormone disruptor antibody covalently linked via a graft chain to  
CC the support, which can be used to capture and subsequently recover the  
CC substances of interest. The present invention provides a method for  
CC selectively and efficiently concentrating hormone disruptors including  
CC alkylphenols, resin components, chlorophenols and female, male or thyroid  
CC hormones from environmental samples. In particular, the method is useful  
CC for the immunological isolation, concentration or clean-up of such trace  
CC hormone disruptors that occur in river water, such that it is a method  
CC applicable for environmental protection and the analytical sciences. This  
CC polypeptide is a murine hormone disruptor antibody (bcFv) protein  
CC sequence of the invention.  
XX  
SQ Sequence 218 AA;  
  
Query Match 96.0%; Score 72; DB 8; Length 218;  
Best Local Similarity 93.8%; Pred. No. 0.00016;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KSSQSLSSRTRKKNYL 16  
|||||:|||||  
Db 24 KSSQSLNSRTRKKNYL 39  
  
RESULT 5  
AAR76086  
ID AAR76086 standard; peptide; 219 AA.  
XX  
AC AAR76086;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX  
DE MAb 55.1 light chain.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.  
XX  
OS Mus sp.  
XX  
PN WO9515382-A1.  
XX  
PD 08-JUN-1995.  
XX  
PF 29-NOV-1994; 94WO-GB002610.  
XX  
PR 03-DEC-1993; 93GB-00024819.  
PR 03-JUN-1994; 94GB-00011089.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;  
XX  
DR WPI; 1995-215262/28.  
XX

PT Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.  
XX  
PS Claim 3; Page 98; 121pp; English.  
XX  
CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
CC of the heavy (AAR76085) and light (AAR76086) chains of MAb 55.1 (ECACC  
CC 93081901), which recognises the colorectal tumor-associated antigen  
CC CA55.1. It is optionally humanized and in the form F(ab')<sub>2</sub>, F(ab)', Fab,  
CC Fv, bcFv or V-min, and is produced in transgenic animals or plants.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 219 AA;  
  
Query Match 96.0%; Score 72; DB 2; Length 219;  
Best Local Similarity 93.8%; Pred. No. 0.00016;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KSSQSLSSRTRKKNYL 16  
|||||:|||||  
Db 24 KSSQSLNSRTRKKNYL 39  
  
RESULT 6  
AAR76087  
ID AAR76087 standard; protein; 239 AA.  
XX  
AC AAR76087;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX  
DE MAb 55.1 light chain.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Protein 21..239  
FT /label= Mat protein  
FT /note= "claim 3, page 98"  
XX  
PN WO9515382-A1.  
XX  
PD 08-JUN-1995.  
XX  
PF 29-NOV-1994; 94WO-GB002610.  
XX  
PR 03-DEC-1993; 93GB-00024819.  
PR 03-JUN-1994; 94GB-00011089.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;  
XX  
DR WPI; 1995-215262/28.  
DR N-PSDB; AAQ94036.  
XX  
PT Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.  
XX  
PS Disclosure; Fig 16; 121pp; English.  
XX

CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, scFv or V-mu  
CC humanized 55.1 constructs have been expressed in myeloma cells and E.  
CC coli. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 239 AA;

Query Match 96.0%; Score 72; DB 2; Length 239;  
Best Local Similarity 93.8%; Pred. No. 0.00018;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| | | | | : | | | | |  
44 KSSQSLSSRTRKNYL 59

RESULT 7  
ADR59117  
ID ADR59117 standard; protein; 244 AA.

XX ADR59117;

DT 18-NOV-2004 (first entry)

DE Anti-K88/K99 antibody related protein, SEQ ID 68.

KW Gastrointestinal; antibody; heavy chain; light chain; variable region;  
KW enterotoxigenic Escherichia coli; ETEC; K88 antigen; K99 antigen;  
KW animal food; enteric disease.

OS Mus sp.

PN WO2004074491-A2.

PD 02-SEP-2004.

PF 16-FEB-2004; 2004WO-EP001427.

PR 18-FEB-2003; 2003US-0448429P.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI Brown D, Campos M, Dalmia B, Demarest S, Hansen G, Heifetz PB;

DR WPI; 2004-635583/61.

PT Novel immunoglobulin heavy chain comprising bovine CH3 or CH2 domain,  
PT murine CH2CH3 domain or human CH2CH3 domain, useful in treatment or  
PT prevention of enteric disease in animal.

PS Claim 58; SEQ ID NO 68; 165pp; English.

CC The present invention relates to coding sequences for mammalian antibody  
CC heavy and light chains directed against enterotoxigenic Escherichia coli  
CC (ETEC), in particular, ETEC of a strain possessing the K88 or K99  
CC antigen. The heavy and light chain sequences are useful for producing  
CC transgenic plants, which express the K88 or K99 antibody. The transgenic  
CC plants are useful for producing animal feed, food product, animal feed  
CC additive, feed pre-mix or nutritional supplement and are also useful for  
CC treating or preventing enteric disease in an animal. The present sequence  
CC was used in an example from the invention.

SQ Sequence 244 AA;

Query Match 96.0%; Score 72; DB 8; Length 244;  
Best Local Similarity 93.8%; Pred. No. 0.00018;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| | | | | : | | | | |  
43 KSSQSLSSRTRKNYL 58

RESULT 8  
AAW82743  
ID AAW82743 standard; protein; 288 AA.

XX AAW82743;

DT 10-MAY-1999 (first entry)

DE Fusion protein PNG4/55.1scFv/CPG2 R6/del EcORI.

KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;  
KW inflammation; rheumatoid arthritis; antibody; prodrug therapy system.

OS Synthetic.

PN WO9851787-A2.

PD 19-NOV-1998.

PF 05-MAY-1998; 98WO-GB001294.

PR 10-MAY-1997; 97GB-00009421.

PA (ZENE ) ZENECA LTD.

PI Emery SC, Blakey DC;

DR WPI; 1999-059700/05.

DR N-PSDB; AAV72064.

PT New gene construct expressing conjugate of targeting agent and prodrug-  
PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
PT drug in vivo, especially for treatment of cancer.

PS Example 15; Page 82; 100pp; English.

CC This sequence is a used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
CC and (B) is directed to leave the cell for selective localisation at a  
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
CC site, then administration of (III) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme prodrug therapy  
CC system

SQ Sequence 288 AA;

Query Match 96.0%; Score 72; DB 2; Length 288;  
Best Local Similarity 93.8%; Pred. No. 0.00022;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| | | | | : | | | | |  
Db 182 KSSQSLSSRTRKNYL 197

RESULT 9  
AAW82742

ID AAW82742 standard; protein; 673 AA.

XX AAW82742;

DT 10-MAY-1999 (first entry)

DE Plasmid PNG4/55.1scFv/CPG2 R6 protein.

KW Conjugate; cell targeting; cytotoxic drug; prodrug-converting enzyme;  
KW cell surface antigen; treatment; cancer; inflammation; antibody;



KM rheumatoid arthritis; prodrug therapy system.  
XX  
OS Synthetic.  
XX  
PN WO9851787-A2.  
XX  
PD 19-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-GB001294.  
XX  
PR 10-MAY-1997; 97GB-00009421.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Emery SC, Blakey DC;  
XX  
DR WPI; 1999-059700/05.  
DR N-PSDB; AAV72059.  
XX  
PT New gene construct expressing conjugate of targeting agent and produg-  
PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
PT drug in vivo, especially for treatment of cancer.  
XX  
PS Example 14; Page 78-79; 100pp; English.  
XX  
CC This sequence is used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
CC targeting group (I) and a heterologous produg-converting enzyme (II),  
CC and (B) is directed to leave the cell for selective localisation at a  
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
CC site, then administration of (III) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme produg therapy  
CC system  
XX  
SQ Sequence 673 AA;  
SQ  
Query Match 96.0%; Score 72; DB 2; Length 673;  
Best Local Similarity 93.8%; Pred. No. 0.00059;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KSSQSLSSRRTRKNYL 16  
Db 179 KSSQSLNSRRTRKNYL 194  
RESULT 10  
AAB07951  
ID AAB07951 standard; peptide; 17 AA.  
XX  
AC AAB07951;  
XX  
DT 14-NOV-2000 (first entry)  
XX  
DE CDR1 sequence from an antibody with affinity for B7 molecules.  
XX  
KM Complementarity determining region; CDR; antibody; B7 molecule; B7-1;  
KM B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;  
KM inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;  
KM insulinitis; asthma; arthritis; inflammatory bowel disease; cancer;  
KM inflammatory dermatitis; multiple sclerosis; transplant rejection;  
KM proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;  
KM thalassemia; aplastic anaemia; myeloid dysplasia syndrome.  
XX  
OS Mus sp.  
XX  
PN WO200047625-A2.  
XX  
PD 17-AUG-2000.  
XX  
PF 09-FEB-2000; 2000WO-US003303.

XX  
PR 12-FEB-1999; 99US-00249011.  
PR 24-JUN-1999; 99US-00339596.  
XX  
XX (GEMY ) GENETICS INST INC.  
XX  
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
XX  
DR WPI; 2000-524532/47.  
XX  
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
PT modulates immune responses and can therefore treat e.g. autoimmune  
PT diseases, infectious diseases.  
XX  
XX  
PS Disclosure; Page 28; 162pp; English.  
XX  
CC The present sequence represents a complementarity determining region  
CC (CDR) 1 from the light chains of an murine antibody with having a binding  
CC specificity to B7-2 molecules. The sequence is used to construct  
CC humanized immunoglobulins, which comprise an antigen binding region of  
CC non-human origin and a portion of a human immunoglobulin. The humanized  
CC immunoglobulins are useful for treating autoimmune diseases, infectious  
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
CC also useful for treating a transplant recipient or preventing transplant  
CC rejection in a transplant recipient, and treating proliferative disease  
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome  
XX  
SQ Sequence 17 AA;  
SQ  
Query Match 90.7%; Score 68; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.5e-05;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KSSQSLSSRRTRKNYL 16  
Db 1 KSSQSLNSRRTRKNYL 16  
RESULT 11  
AAW56520  
ID AAW56520 standard; protein; 110 AA.  
XX  
AC AAW56520;  
XX  
DT 28-SEP-1998 (first entry)  
XX  
DE Anti-DNA IL/IM (H221) VL-JL sequence.  
XX  
KM Intracellular targeting sequence; DNA vaccine; genetic immunisation;  
KM systemic lupus erythematosus; antibody; H221.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FH Region 24..40  
FT /label= CDR-I  
FT Region 56..62  
FT /label= CDR-II  
FT Region 95..102  
FT /label= CDR-III  
XX  
PN WO9817323-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 23-OCT-1997; 97WO-US019545.  
XX

PR 23-OCT-1996; 96US-0029592P.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Williams WV, Madaio M, Weiner DB;  
XX  
DR WPI; 1998-261198/23.  
DR N-PSDB; AAV29839.  
XX  
PT Plasmid encoding immunogenic target protein - used in, e.g. protective or  
PT therapeutic vaccines against allergy, cancer, microbial infection or auto  
PT -immune disease.  
XX  
PS Example 1; Page 31; 84pp; English.  
XX  
CC This polypeptide comprises the VL-JL sequence of anti-DNA IL/IM (H221)  
CC antibody. This antibody binds to murine renal mesangial cells and aortic  
CC endothelial cells, properties associated with pathogenic systemic lupus  
CC erythematosus antibodies. H221 VH and VL DNA regions (see AAV29839-40)  
CC have been amplified by PCR (see AAV29841-54) and used to generate VH and  
CC Fv coding sequences. These were cloned into a genetic immunisation vector  
CC and administered to mice for use in DNA vaccination studies. DNA  
CC inoculation against the H221 VH and Fv regions elicited specific cellular  
CC immune responses, particularly potent cytotoxic T lymphocyte (CTL)  
CC responses, with enhancement in CTL activity by targeting the V region to  
CC the cytosol or to the endoplasmic reticulum (ER). The invention provides  
CC a novel plasmid comprising a sequence that encodes an immunogenic target  
CC protein that includes, or is linked to, an intracellular targeting  
CC sequence (see AAW56512-14) that directs localisation of the target  
CC protein to the lysosome or ER. The novel plasmid is used as a protective  
CC or therapeutic DNA vaccine to immunise against the immunogenic target  
CC protein (claimed)  
XX  
SQ Sequence 110 AA;

Query Match 90.7%; Score 68; DB 2; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00039;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
||| | : ||| | | |  
Db 24 KSSQSLFNSRTRKNYL 39

RESULT 12  
ABR42303  
ID ABR42303 standard; protein; 111 AA.  
XX  
AC ABR42303;

DT 11-AUG-2003 (first entry)  
XX  
DE Mouse monoclonal antibody 679 humanised light chain variable region.  
XX  
KW Diabody; antibody; humanised; histamine-succinyl-glycyl; HSG;  
KW affinity enhancement system; tumour; targeting.  
XX  
OS Mus sp.

XX Key Location/Qualifiers  
FH Region 1. .30  
FT /label= FR1  
FT Misc-difference 5 /note= "wild-type Ser substituted by Thr"  
FT Misc-difference 18 /note= "wild-type Lys substituted by Arg"  
FT Misc-difference 21 /note= "wild-type Met substituted by Leu"  
FT Region 31. .35  
FT /label= CDR1  
FT Region 36. .49  
FT /label= FR2  
FT Region 50. .66

FT /label= CDR2  
FT Region 67. .98  
FT /label= FR3  
FT Misc-difference 68 /note= "wild-type Thr substituted by Ser"  
FT Region 99. .108  
FT /label= CDR3  
FT Region 109. .119  
FT /label= FR3  
XX  
XX WO2003033653-A2.  
PN  
XX  
XX 24-APR-2003.  
PD  
XX  
XX 15-OCT-2002; 2002WO-US032717.  
PF  
XX  
XX 15-OCT-2001; 2001US-0328835P.  
PR  
XX 21-DEC-2001; 2001US-0341881P.  
XX  
PA (IMMU-) IMMUNOMEDICS INC.  
PA (IBCP-) IBC PHARM.  
XX  
PI Chang CK, Rossi E;  
XX  
DR WPI; 2003-393513/37.  
XX

PT New kit comprising a multivalent, multi-specific binding protein and a  
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent  
PT for treating cancer, and cardiovascular, immune, inflammatory, or  
PT infectious diseases.  
XX  
XX  
PS Disclosure; Fig 20; 87pp; English.  
XX

CC The present sequence is the protein sequence of a humanised version of  
CC the light chain variable region (VL) of murine monoclonal antibody 679  
CC (see ABR42302). This antibody binds with high affinity to molecules  
CC containing the moiety histamine-succinyl-glycyl (HSG). The present  
CC humanised version of 679 VL has HSG binding affinity comparable to that  
CC of the murine form. It was utilised in bispecific diabody constructs of  
CC the invention (see ABR42297-99). These bispecific diabodies comprise an  
CC HSG binding site and a carcinoembryonic antigen (CEA) binding site. They  
CC are produced via recombinant DNA technology and create a novel affinity  
CC enhancement system that shows specific affinity for HSG and CEA. The  
CC diabodies pre-target CEA positive tumours for subsequent specific  
CC delivery of therapeutic radiolabels carried by HSG-carrying peptides.  
CC Cancer, autoimmune diseases, infectious disease, cardiovascular diseases  
CC and inflammatory diseases can be detected or treated using the methods of  
CC the invention  
XX  
XX  
SQ Sequence 111 AA;

Query Match 90.7%; Score 68; DB 6; Length 111;  
Best Local Similarity 87.5%; Pred. No. 0.00039;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
||| | : ||| | | |  
Db 24 KSSQSLFNSRTRKNYL 39

RESULT 13  
ABR42302  
ID ABR42302 standard; protein; 111 AA.  
XX  
AC ABR42302;

DT 11-AUG-2003 (first entry)  
XX  
DE Mouse monoclonal antibody 679 light chain variable region.  
XX  
KW Diabody; antibody; histamine-succinyl-glycyl; HSG; mouse;  
KW affinity enhancement system; tumour; targeting.  
XX

OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..23
FT		/label= FR1
FT	Region	24..40
FT		/label= CDR1
FT	Region	41..54
FT		/label= FR2
FT	Region	55..61
FT		/label= CDR2
FT	Region	62..91
FT		/label= FR3
FT	Region	92..100
FT		/label= CDR3
FT	Region	101..111
FT		/label= FR3
XX		
PN	WO2003033653-A2.	
XX		
PD	24-APR-2003.	
XX		
PF	15-OCT-2002; 2002WO-US032717.	
XX		
PR	15-OCT-2001; 2001US-0328835P.	
PR	21-DEC-2001; 2001US-0341881P.	
XX		
PA	(IMMU-) IMMUNOMEDICS INC.	
PA	(IBC-) IBC PHARM.	
XX		
PI	Chang CK, Rossi E;	
XX		
DR	WPI; 2003-393513/37.	
XX		
PT	New kit comprising a multivalent, multi-specific binding protein and a	
PT	carrier molecule, useful for delivering a diagnostic/therapeutic agent	
PT	for treating cancer, and cardiovascular, immune, inflammatory, or	
PT	infectious diseases.	
XX		
PS	Disclosure; Fig 20; 87pp; English.	
XX		
CC	The present sequence is the protein sequence of the light chain variable	
CC	region (VL) of murine monoclonal antibody 679. This antibody binds with	
CC	high affinity to molecules containing the moiety histamine-succinyl-	
CC	glycyl (HSG). A humanised version of 679 VL has been generated (see	
CC	ABR42303) that has HSG binding affinity comparable to that of the murine	
CC	form. It was utilised in bispecific diabody constructs of the invention	
CC	(see ABR42297-99). These bispecific diabodies comprise an HSG binding	
CC	site and a carcinoembryonic antigen (CEA) binding site. They are produced	
CC	via recombinant DNA technology and create a novel affinity enhancement	
CC	system that shows specific affinity for HSG and CEA. The diabodies pre-	
CC	target CEA positive tumours for subsequent specific delivery of	
CC	therapeutic radioisotopes carried by HSG-carrying peptides. Cancer,	
CC	autoimmune diseases, infectious disease, cardiovascular diseases and	
CC	inflammatory diseases can be detected or treated using the methods of the	
CC	invention	
XX		
SQ	Sequence 111 AA;	
	Query Match 90.7%; Score 68; DB 6; Length 111;	
	Best Local Similarity 87.5%; Pred. No. 0.00039;	
	Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Oy	1 KSSQSLSSRRKNYL 16	
	:	
Db	24 KSSQSLFNSRRKNYL 39	
RESULT 14		
ID	ADC03128 standard; protein; 113 AA.	
XX		
AC	ADC03128;	

XX		
DT	18-DEC-2003 (first entry)	
XX		
DB	Colon specific antigen-p mucin murine antibody 679 V <sub>K</sub> protein.	
XX		
KW	cytostatic; antitumour; antibody; colon specific antigen-p mucin;	
KW	hapten binding site; immunconjugate; close-range lesion; tumour; ovary;	
KW	thymus; parathyroid; spleen; carcinoma; gastrointestinal cancer;	
KW	colorectal cancer; pancreatic cancer; ovarian cancer.	
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	24..40
FT		/note
FT		/note= "complementarity determining region 1"
FT	Domain	56..62
FT		/note
FT		/note= "complementarity determining region 2"
FT	Domain	95..102
FT		/note
FT		/note= "complementarity determining region 3"
XX		
PN	WO200282041-A2.	
XX		
PD	17-OCT-2002.	
XX		
PF	03-APR-2002; 2002WO-US010235.	
XX		
PR	03-APR-2001; 2001US-00823746.	
XX		
PA	(IMMU-) IMMUNOMEDICS INC.	
XX		
PI	Hansen HJ, Griffiths GL, Leung S, McBride WJ, Qu Z;	
PI	Goldenberg DM;	
XX		
DR	WPI; 2003-167089/16.	
DR	N-PSDB; ADC03179.	
XX		
PT	Novel multivalent, multispecific antibody for detecting/treating tumors	
PT	expressing colon specific antigen-p mucin in mammal, comprises antigen	
PT	and hapten binding sites.	
XX		
PS	Disclosure; Fig 1; 202pp; English.	
XX		
CC	The invention relates to a multivalent, multispecific antibody or its	
CC	fragment comprising one more antigen binding sites having affinity	
CC	towards colon specific antigen-p mucin (CSAp) target antigen and one or	
CC	more hapten binding sites having affinity towards hapten molecules. The	
CC	antibody is useful for screening a targetable conjugate. A therapeutic	
CC	immunconjugate comprising the antibody is useful for detecting close-	
CC	range lesion. The antibody or immunconjugate are also useful for	
CC	delivering a diagnostic/detection or therapeutic agent, or their	
CC	combination, to a target. The antibody or a targetable conjugate are	
CC	useful for detecting or treating tumours expressing CSAp in a mammal, for	
CC	imaging malignant tissue or normal tissue or cells in a mammal expressing	
CC	CSAp, where the normal tissue is from ovary, thymus, parathyroid or	
CC	spleen, for intraoperatively identifying/disclosing the diseased tissues	
CC	expressing CSAp in a subject, and for endoscopic identification of	
CC	diseased tissues expressing CSAp. They are also useful for intravascular	
CC	identification of diseased tissues expressing CSAp, for detecting lesions	
CC	during an endoscopic, laparoscopic, intravascular catheter or surgical	
CC	procedure, and for detecting and treating target cells, tissues or	
CC	pathogens in a mammal. A method using the antibody is useful for	
CC	diagnosing or detecting a malignancy in a subject, where the malignancy	
CC	is carcinoma, gastrointestinal cancer, colorectal or pancreatic cancer or	
CC	ovarian cancer, the subject is human or a domestic pet. This sequence	
CC	represents one of the antibodies of the invention.	
XX		
SQ	Sequence 113 AA;	
	Query Match 90.7%; Score 68; DB 7; Length 113;	
	Best Local Similarity 87.5%; Pred. No. 0.0004;	

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 KSSQSLSSRTRKNYL 16  
          |||||:|||||  
Db 24 KSSQSLNSRTRKNYL 39

RESULT 15  
AD032150  
ID AD032150 standard; protein; 115 AA.  
XX  
AC AD032150;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Mouse anti-CD3 antibody light chain homologous protein SEQ ID NO:66.  
XX  
KW anti-CD3 antibody; epitope-binding fragment;  
KW complementarity-determining region; CDR; immunconjugate; cytostatic;  
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.  
XX  
OS Mus musculus.  
XX  
PN WO2004043344-A2.  
XX  
PD 27-MAY-2004.  
XX  
PF 05-NOV-2003; 2003WO-US032737.  
XX  
PR 07-NOV-2002; 2002US-0424332P.  
XX  
PA (IMMU-) IMMUNOGEN INC.  
XX  
PI Hoffee MG, Tavares D, Lutz RJ;  
XX  
DR WPI; 2004-411619/38.  
XX  
PT New antibodies that bind to CD33, useful for treating a disease  
PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
PT or chronic myeloid leukemia.  
XX  
PS Example 3; SEQ ID NO 66; 124pp; English.  
XX

CC The present invention describes an isolated anti-CD33 antibody or its  
CC epitope-binding fragment comprising: (a) at least one complementarity-  
CC determining region (CDR); or (b) at least heavy chain variable region  
CC comprising 3 CDRs, and at least one light chain variable region, where  
CC the CDR has the ability to bind CD33. Also described: (1) an  
CC immunconjugate comprising the antibody or its epitope-binding fragment  
CC linked to a drug or produg; (2) a composition comprising the antibody or  
CC epitope-binding fragment and a drug or produg; (3) a pharmaceutical  
CC composition comprising the immunconjugate, composition or the antibody  
CC defined above, or its epitope-binding fragment, and a pharmaceutical  
CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
CC growth of a cell expressing CD33 by contacting the cell with the above  
CC defined antibody or its epitope-binding fragment, immunconjugate, or  
CC (pharmaceutical) composition; (6) determining whether a biological sample  
CC contains a myelogenous cancer cell; (7) an improved antibody or its  
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
CC polynucleotide encoding the antibody or its epitope-binding fragment  
CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
CC chain of the antibody defined above or its epitope-binding fragment; (10)  
CC a recombinant vector comprising the polynucleotide; (11) a host cell  
CC transformed with the recombinant vector; (12) producing an antibody or  
CC its epitope-binding fragment having the ability to bind CD33; and (13)  
CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
CC cytostatic activity. The antibody or its epitope-binding fragment,  
CC immunconjugate, composition can be used for treating a subject having a  
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
CC It can also be used for inhibiting the growth of cells expressing CD33,  
CC

CC and for in vivo imaging or as affinity purification agents. The present  
CC sequence represents a mouse anti-CD33 antibody light chain homologous  
CC amino acid sequence, which is used in an example from the present  
CC invention.  
XX  
SQ Sequence 115 AA;

Query Match 90.7%; Score 68; DB 8; Length 115;  
Best Local Similarity 87.5%; Pred. No. 0.00041;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KSSQSLSSRTRKNYL 16  
          |||||:|||||  
Db 24 KSSQSLNSRTRKNYL 39

Search completed: March 1, 2005, 17:36:07  
Job time : 121.631 secs



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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 31.2615 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRRKNYL 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	96.0	17	1 US-08-353-400-30	Sequence 30, Appl
2	72	96.0	219	1 US-08-353-400-34	Sequence 34, Appl
3	72	96.0	239	1 US-08-353-400-37	Sequence 37, Appl
4	72	96.0	288	3 US-09-423-439-38	Sequence 38, Appl
5	72	96.0	673	3 US-09-423-439-32	Sequence 32, Appl
6	68	90.7	17	4 US-09-627-896B-16	Sequence 16, Appl
7	68	90.7	110	3 US-08-957-001B-5	Sequence 5, Appl
8	68	90.7	110	3 US-08-957-001B-24	Sequence 24, Appl
9	68	90.7	110	3 US-09-496-301-5	Sequence 24, Appl
10	68	90.7	110	3 US-09-496-301-24	Sequence 24, Appl
11	68	90.7	132	4 US-09-627-896B-4	Sequence 4, Appl
12	68	90.7	132	4 US-09-627-896B-8	Sequence 8, Appl
13	68	90.7	239	4 US-09-627-896B-22	Sequence 22, Appl
14	65	86.7	265	2 US-08-403-853-16	Sequence 16, Appl
15	63	84.0	109	2 US-08-308-494A-23	Sequence 23, Appl
16	60	80.0	113	4 US-09-301-593-2	Sequence 4, Appl
17	60	80.0	113	4 US-09-301-593-4	Sequence 4, Appl
18	60	80.0	113	4 US-09-301-593-6	Sequence 6, Appl
19	60	80.0	113	4 US-09-301-593-32	Sequence 32, Appl
20	60	80.0	113	4 US-09-301-593-33	Sequence 33, Appl
21	60	80.0	113	4 US-09-301-593-34	Sequence 34, Appl
22	60	80.0	114	3 US-08-929-856-66	Sequence 66, Appl
23	60	80.0	133	4 US-09-301-593-24	Sequence 24, Appl
24	60	80.0	220	4 US-09-301-593-17	Sequence 17, Appl
25	60	80.0	240	4 US-09-301-593-28	Sequence 28, Appl
26	60	80.0	240	4 US-09-301-593-36	Sequence 36, Appl
27	57	76.0	113	3 US-08-579-378A-5	Sequence 5, Appl

28	57	76.0	113	3 US-08-579-378A-6	Sequence 6, Appl
29	57	76.0	113	5 PCT-US93-11612-5	Sequence 5, Appl
30	57	76.0	113	5 PCT-US93-11612-6	Sequence 6, Appl
31	57	76.0	113	3 US-08-579-378A-2	Sequence 2, Appl
32	57	76.0	113	3 US-08-579-378A-10	Sequence 10, Appl
33	57	76.0	113	5 PCT-US93-11612-2	Sequence 2, Appl
34	57	76.0	113	5 PCT-US93-11612-10	Sequence 10, Appl
35	56	74.7	17	1 US-08-467-420A-10	Sequence 10, Appl
36	56	74.7	17	1 US-08-470-110A-10	Sequence 10, Appl
37	56	74.7	17	1 US-08-667-769A-10	Sequence 10, Appl
38	56	74.7	17	2 US-08-940-371-10	Sequence 10, Appl
39	56	74.7	17	3 US-08-637-647-10	Sequence 10, Appl
40	56	74.7	17	4 US-09-563-222C-26	Sequence 26, Appl
41	56	74.7	17	5 PCT-US95-17082A-10	Sequence 10, Appl
42	56	74.7	105	1 US-08-467-420A-16	Sequence 16, Appl
43	56	74.7	105	1 US-08-470-110A-16	Sequence 16, Appl
44	56	74.7	105	2 US-08-940-371-16	Sequence 16, Appl
45	56	74.7	105	3 US-08-637-647-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-353-400-30  
; Sequence 30, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-353-400-30  
  
Query Match 96.0%; Score 72; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 4.7e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KSSQSLSSRRKNYL 16  
|||  
Db 1 KSSQSLSSRRKNYL 16  
  
RESULT 2  
US-08-353-400-34  
; Sequence 34, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:



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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-34
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Query Match 96.0%; Score 72; DB 1; Length 219;
Best Local Similarity 93.8%; Pred. No. 6.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 KSSQSLSSRTRKNYL 16
| | | | | : | | | | |
Db 24 KSSQSLNSRTRKNYL 39
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```
RESULT 3
US-08-353-400-37
; Sequence 37, Application US/08353400
; Patent No. 565357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-37
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Query Match 96.0%; Score 72; DB 1; Length 239;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KSSQSLSSRTRKNYL 16
| | | | | : | | | | |
Db 44 KSSQSLNSRTRKNYL 59
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RESULT 4
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
```

```
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
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; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38
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Query Match 96.0%; Score 72; DB 3; Length 288;
Best Local Similarity 93.8%; Pred. No. 9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 KSSQSLSSRTRKNYL 16
| | | | | : | | | | |
Db 182 KSSQSLNSRTRKNYL 197
```

```
RESULT 5
US-09-423-439-32
; Sequence 32, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
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```
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 32:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 673 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match          96.0%; Score 72; DB 3; Length 673;
Best Local Similarity 93.8%; Pred. No. 0.00022;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KSSQSLSSRTKKNYL 16
        |||||:|||||
Db      179 KSSQSLSSRTKKNYL 194

RESULT 6
US-09-627-896B-16
; Sequence 16, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARENNO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627, 896B
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR1 of humanized
; OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-627-896B-16

Query Match          90.7%; Score 68; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KSSQSLSSRTKKNYL 16
        |||||:|||||
Db      1 KSSQSLSSRTKKNYL 16

RESULT 7
US-08-957-001B-5
; Sequence 5, Application US/08957001B
; Patent No. 6228621
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Madaio, Michael
```

```
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: IMPROVED VACCINES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: windows
; SOFTWARE: wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957, 001B
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029, 592
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; APPLICANT: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-3303
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 110 amino acids
;   TYPE: amino acid
;   TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-957-001B-5

Query Match          90.7%; Score 68; DB 3; Length 110;
Best Local Similarity 87.5%; Pred. No. 0.00016;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSSQSLSSRTKKNYL 16
        |||||:|||||
Db      24 KSSQSLSSRTKKNYL 39

RESULT 8
US-08-957-001B-24
; Sequence 24, Application US/08957001B
; Patent No. 6228621
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Madaio, Michael
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: IMPROVED VACCINES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: windows
; SOFTWARE: wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957, 001B
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 424
```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-957-001B-24

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16  
|||||:|||||  
Db 24 KSSQSLFNSRTKKNYL 39

RESULT 9  
US-09-496-301-5  
Sequence 5, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madaio, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide

US-09-496-301-5

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16  
|||||:|||||  
Db 24 KSSQSLFNSRTKKNYL 39

RESULT 10

US-09-496-301-24

Sequence 24, Application US/09496301

Patent No. 6248565

GENERAL INFORMATION:

APPLICANT: Williams, William V.

APPLICANT: Madaio, Michael

APPLICANT: Weiner, David B.

TITLE OF INVENTION: IMPROVED VACCINES

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565r1s

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: windows

SOFTWARE: wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/496,301

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/957,001

FILING DATE: 23-OCT-1997

APPLICATION NUMBER: US 60/029,592

FILING DATE: 23-OCT-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: UPN-3303

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-496-301-24

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16  
|||||:|||||  
Db 24 KSSQSLFNSRTKKNYL 39

RESULT 11

US-09-627-896B-4

Sequence 4, Application US/09627896B

Patent No. 6827934

GENERAL INFORMATION:

APPLICANT: CO, MAN SUNG

```

; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARENNO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627, 896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: Anti-B7-2 light chain
US-09-627-896B-4
```

```

Query Match      90.7%; Score 68; DB 4; Length 132;
Best Local Similarity 87.5%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KSSQSLSSRTKRYL 16
        |||||:||||:|
DB      44 KSSQSLNSRTRENYL 59
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```

RESULT 12
US-09-627-896B-8
; Sequence 8, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARENNO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627, 896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-627-896B-8
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```

Query Match      90.7%; Score 68; DB 4; Length 132;
Best Local Similarity 87.5%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KSSQSLSSRTKRYL 16
        |||||:||||:|
DB      44 KSSQSLNSRTRENYL 59
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```

RESULT 13
US-09-627-896B-22
; Sequence 22, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARENNO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627, 896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: 3D1 light chain
US-09-627-896B-22
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Query Match      90.7%; Score 68; DB 4; Length 239;
Best Local Similarity 87.5%; Pred. No. 0.00037;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KSSQSLSSRTKRYL 16
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DB      44 KSSQSLNSRTRENYL 59
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RESULT 14
US-08-403-853-16
; Sequence 16, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403, 853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-403-853-16
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Query Match      86.7%; Score 65; DB 2; Length 265;
Best Local Similarity 81.2%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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OY      1 KSSQSLSSRTRKNYL 16
      :|||||:|||||
Db      165 RSSQSLFNSRTRKNYL 180
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## RESULT 15

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US-08-308-494A-23
; Sequence 23, Application US/08308494A
; Patent No. 5959083
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; GENERAL INFORMATION:
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```
; APPLICANT: Bobslet, Klaus
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```
; APPLICANT: Seeman, Gerhard
```

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; TITLE OF INVENTION: Tetravalent Bispecific Receptors, The
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; TITLE OF INVENTION: Preparation and Use Thereof
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```
; NUMBER OF SEQUENCES: 24
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; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
```

```
; ADDRESSEE: Dunner
```

```
; STREET: 1300 I Street, N.W., Suite 700
```

```
; CITY: Washington
```

```
; STATE: D.C.
```

```
; COUNTRY: USA
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; ZIP: 20005-3315
```

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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/308,494A
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; FILING DATE: 21-SEP-1994
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; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/891,739
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; FILING DATE: 01-JUN-1992
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; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: DE P4118120.4
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; FILING DATE: 03-JUN-1991
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; ATTORNEY/AGENT INFORMATION:
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```
; NAME: Kulik, David J.
```

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; REGISTRATION NUMBER: 36,576
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; REFERENCE/DOCKET NUMBER: 05552-1186-02000
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; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 202-408-4000
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; TELEFAX: 202-408-4400
```

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; INFORMATION FOR SEQ ID NO: 23:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-308-494A-23
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Best Local Similarity 87.5%; Pred. No. 0.0012;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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      :|||||:|||||
Db      21 KSSQSLSSRTRKNYL 36
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Search completed: March 1, 2005, 17:46:57
Job time : 32.2615 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 85.6615 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRTRKNYL 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	16	14	US-10-071-962-18 Sequence 18, Appl
2	68	90.7	17	9	US-09-249-011A-16 Sequence 16, Appl
3	68	90.7	113	14	US-10-270-071-7 Sequence 7, Appli
4	68	90.7	113	14	US-10-270-071-8 Sequence 8, Appli
5	68	90.7	132	9	US-09-249-011A-4 Sequence 4, Appli
6	68	90.7	132	9	US-09-249-011A-8 Sequence 8, Appli
7	68	90.7	239	9	US-09-249-011A-22 Sequence 22, Appl
8	68	90.7	267	14	US-10-270-071-22 Sequence 22, Appl
9	68	90.7	267	14	US-10-270-071-26 Sequence 26, Appl
10	68	90.7	267	14	US-10-270-071-30 Sequence 30, Appl
11	68	90.7	267	14	US-10-270-071-36 Sequence 36, Appl
12	68	90.7	268	14	US-10-270-071-10 Sequence 10, Appl
13	68	90.7	268	14	US-10-270-071-12 Sequence 12, Appl

14	68	90.7	268	14	US-10-270-071-14	Sequence 14, Appl
15	68	90.7	268	14	US-10-270-071-16	Sequence 16, Appl
16	68	90.7	268	14	US-10-270-071-32	Sequence 32, Appl
17	68	90.7	268	14	US-10-328-190-2	Sequence 2, Appli
18	68	90.7	268	14	US-10-328-190-4	Sequence 4, Appli
19	68	90.7	358	16	US-10-829-388-12	Sequence 12, Appl
20	68	90.7	363	16	US-10-829-388-2	Sequence 2, Appli
21	68	90.7	391	14	US-10-328-190-14	Sequence 14, Appl
22	63	84.0	17	10	US-09-995-529-73	Sequence 73, Appl
23	63	84.0	17	11	US-09-995-529-73	Sequence 73, Appl
24	60	80.0	113	9	US-09-301-593-2	Sequence 2, Appli
25	60	80.0	113	9	US-09-301-593-4	Sequence 4, Appli
26	60	80.0	113	9	US-09-301-593-6	Sequence 6, Appli
27	60	80.0	113	9	US-09-301-593-32	Sequence 32, Appl
28	60	80.0	113	9	US-09-301-593-33	Sequence 33, Appl
29	60	80.0	113	9	US-09-301-593-34	Sequence 34, Appl
30	60	80.0	113	10	US-09-215-163-42	Sequence 42, Appl
31	60	80.0	113	14	US-10-121-464-2	Sequence 2, Appli
32	60	80.0	113	14	US-10-121-464-4	Sequence 4, Appli
33	60	80.0	113	14	US-10-121-464-6	Sequence 6, Appli
34	60	80.0	113	14	US-10-159-006-2	Sequence 2, Appli
35	60	80.0	113	14	US-10-159-006-4	Sequence 4, Appli
36	60	80.0	113	14	US-10-159-006-6	Sequence 6, Appli
37	60	80.0	113	14	US-10-159-006-32	Sequence 32, Appl
38	60	80.0	113	14	US-10-159-006-33	Sequence 33, Appl
39	60	80.0	113	14	US-10-159-006-34	Sequence 34, Appl
40	60	80.0	133	9	US-09-301-593-24	Sequence 24, Appl
41	60	80.0	133	14	US-10-159-006-24	Sequence 24, Appl
42	60	80.0	220	9	US-09-301-593-17	Sequence 17, Appl
43	60	80.0	220	14	US-10-159-006-17	Sequence 17, Appl
44	60	80.0	240	9	US-09-301-593-28	Sequence 28, Appl
45	60	80.0	240	9	US-09-301-593-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1  
US-10-071-962-18  
; Sequence 18, Application US/10071962  
; Publication No. US20030170237A1  
; GENERAL INFORMATION:  
; APPLICANT: BauFu Ni  
; APPLICANT: Bill N.C. Sun  
; APPLICANT: Cedily R.Y. Sun  
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
; TITLE OF INVENTION: Screening Method Therefor  
; FILE REFERENCE: 98-3  
; CURRENT APPLICATION NUMBER: US/10/071,962  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US/09/303,155A  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/083,575  
; PRIOR FILING DATE: 1998-04-30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-071-962-18

Query Match 100.0%; Score 75; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KSSQSLSSRTRKNYL 16  
Db 1 KSSQSLSSRTRKNYL 16

RESULT 2  
US-09-249-011A-16

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; Sequence 16, Application US/09249011A
; Patent No. US2002017685A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249, 011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR1 of humanized
; OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-249-011A-16
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Query Match          90.7%; Score 68; DB 9; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.0001;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KSSQSLSSRTRKNYL 16
        |||||:|||||:||||
Db       1 KSSQSLNSRTRKNYL 16
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## RESULT 3

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US-10-270-071-7
; Sequence 7, Application US/10270071
; Publication No. US2003011333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270, 071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328, 835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341, 881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of m679VK
US-10-270-071-7
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Query Match          90.7%; Score 68; DB 14; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00074;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 KSSQSLSSRTRKNYL 16
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Db       24 KSSQSLFNSRTRKNYL 39
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RESULT 4
US-10-270-071-8
; Sequence 8, Application US/10270071
; Publication No. US2003011333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270, 071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328, 835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341, 881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of h679VK
US-10-270-071-8
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Query Match          90.7%; Score 68; DB 14; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00074;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 KSSQSLSSRTRKNYL 16
        |||||:|||||:||||
Db       24 KSSQSLFNSRTRKNYL 39
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## RESULT 5

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US-09-249-011A-4
; Sequence 4, Application US/09249011A
; Patent No. US2002017685A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249, 011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: Anti-B7-2 light chain
US-09-249-011A-4
```

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Query Match          90.7%; Score 68; DB 9; Length 132;
Best Local Similarity 87.5%; Pred. No. 0.00088;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 KSSQSLSSRTRKNYL 16
        |||||:|||||:||||
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Db 44 KSSQSLNSRTRENYL 59

RESULT 6

US-09-249-011A-8

; Sequence 8, Application US/09249011A  
; Patent No. US20020176855A1  
; GENERAL INFORMATION:

; APPLICANT: CO, MAN SUNG

; APPLICANT: VASQUEZ, MAXIMILIANO

; APPLICANT: CARRENO, BEATRIZ

; APPLICANT: CELNIKER, ABBIE CHERYL

; APPLICANT: COLLINS, MARY

; APPLICANT: GOLDMAN, SAMUEL

; APPLICANT: GRAY, GARY S.

; APPLICANT: KNIGHT, ANDREA

; APPLICANT: O'HARA, DENISE

; APPLICANT: RUP, BONITA

; APPLICANT: VELDMAN, GEERTRUIDA M.

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS

; TITLE OF INVENTION: OF TREATMENT THEREWITH

; FILE REFERENCE: 08702.0081-00000

; CURRENT APPLICATION NUMBER: US/09/249, 011A

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 132

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Humanized

; OTHER INFORMATION: murine anti-human B7-2 light chain

US-09-249-011A-8

Query Match 90.7%; Score 68; DB 9; Length 132;  
Best Local Similarity 87.5%; Pred. No. 0.00088;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16

Db 44 KSSQSLNSRTRENYL 59

RESULT 7

US-09-249-011A-22

; Sequence 22, Application US/09249011A

; Patent No. US20020176855A1

; GENERAL INFORMATION:

; APPLICANT: CO, MAN SUNG

; APPLICANT: VASQUEZ, MAXIMILIANO

; APPLICANT: CARRENO, BEATRIZ

; APPLICANT: CELNIKER, ABBIE CHERYL

; APPLICANT: COLLINS, MARY

; APPLICANT: GOLDMAN, SAMUEL

; APPLICANT: GRAY, GARY S.

; APPLICANT: KNIGHT, ANDREA

; APPLICANT: O'HARA, DENISE

; APPLICANT: RUP, BONITA

; APPLICANT: VELDMAN, GEERTRUIDA M.

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS

; TITLE OF INVENTION: OF TREATMENT THEREWITH

; FILE REFERENCE: 08702.0081-00000

; CURRENT APPLICATION NUMBER: US/09/249, 011A

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-249-011A-22

Query Match 90.7%; Score 68; DB 9; Length 239;  
Best Local Similarity 87.5%; Pred. No. 0.0016;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16

Db 44 KSSQSLNSRTRENYL 59

RESULT 8

US-10-270-071-22

; Sequence 22, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:

; APPLICANT: ROSSI, EDMUND

; APPLICANT: CHANG, CHIEN-HSING KEN

; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS

; FILE REFERENCE: 042418/0110

; CURRENT APPLICATION NUMBER: US/10/270, 071

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/328, 835

; PRIOR FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 60/341, 881

; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

US-10-270-071-22

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16

Db 170 KSSQSLFNSRTRKNYL 185

RESULT 9

US-10-270-071-26

; Sequence 26, Application US/10270071

; Publication No. US20030113333A1

; GENERAL INFORMATION:

; APPLICANT: ROSSI, EDMUND

; APPLICANT: CHANG, CHIEN-HSING KEN

; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS

; FILE REFERENCE: 042418/0110

; CURRENT APPLICATION NUMBER: US/10/270, 071

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/328, 835

; PRIOR FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 60/341, 881

; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

; OTHER INFORMATION: sequence of polypeptide 2 of Bsl.5

US-10-270-071-26

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||||:|||||  
Db 170 KSSQSLFNSRTRKNYL 185

## RESULT 10

US-10-270-071-30  
; Sequence 30, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-270-071-30

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||||:|||||  
Db 170 KSSQSLFNSRTRKNYL 185

## RESULT 11

US-10-270-071-36  
; Sequence 36, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence for polypeptide 1 of BS1.5H (h679XhMn14 bispecific  
; OTHER INFORMATION: diabody)  
US-10-270-071-36

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16

Db 170 KSSQSLFNSRTRKNYL 185

## RESULT 12

US-10-270-071-10  
; Sequence 10, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence of 679-scFv-L5  
US-10-270-071-10

Query Match 90.7%; Score 68; DB 14; Length 268;  
Best Local Similarity 87.5%; Pred. No. 0.0019;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||||:|||||  
Db 171 KSSQSLFNSRTRKNYL 186

## RESULT 13

US-10-270-071-12  
; Sequence 12, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence of 679-13Q  
US-10-270-071-12

Query Match 90.7%; Score 68; DB 14; Length 268;  
Best Local Similarity 87.5%; Pred. No. 0.0019;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||||:|||||  
Db 171 KSSQSLFNSRTRKNYL 186

## RESULT 14

US-10-270-071-14  
; Sequence 14, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence of 679-C101S  
US-10-270-071-14

## Query Match

90.7%; Score 68; DB 14; Length 268;  
Best Local Similarity 87.5%; Pred. No. 0.0019;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY

1 KSSQSLSSRTRKKNYL 16

Db 171 KSSQSLFNSRTRKKNYL 186

## RESULT 15

US-10-270-071-16  
; Sequence 16, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence of 679 I3Q/C101S  
US-10-270-071-16

## Query Match

90.7%; Score 68; DB 14; Length 268;  
Best Local Similarity 87.5%; Pred. No. 0.0019;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY

1 KSSQSLSSRTRKKNYL 16

Db 171 KSSQSLFNSRTRKKNYL 186

Search completed: March 1, 2005, 17:52:51  
Job time : 86.6615 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 21.6615 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-18

Perfect score: 75

Sequence: 1 KSSQSLSSRRKNYL 16

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	72	96.0	81	2 PH1048	Ig light chain V r
2	72	96.0	101	2 PH1046	Ig light chain V r
3	72	96.0	103	2 PH1047	Ig light chain V r
4	72	96.0	112	2 S43103	Ig kappa chain V-J
5	72	96.0	113	2 PT0408	Ig light chain V r
6	72	96.0	113	2 PT0407	Ig light chain V r
7	72	96.0	120	2 G33932	Ig kappa chain pre
8	71	94.7	103	2 PH1050	Ig light chain V r
9	71	94.7	104	2 PH1101	Ig light chain V r
10	71	94.7	104	2 PH1102	Ig light chain V r
11	71	94.7	104	2 PH1103	Ig light chain V r
12	71	94.7	104	2 PH1104	Ig light chain V r
13	68	90.7	112	2 PL0265	Ig kappa chain V r
14	67	89.3	103	2 PH1051	Ig light chain V r
15	67	89.3	103	2 PH1052	Ig light chain V r
16	66	88.0	111	2 S03304	Ig kappa chain V r
17	64	85.3	97	2 A42575	Ig kappa chain V r
18	63	84.0	94	2 S20648	Ig kappa chain V r
19	63	84.0	113	2 PL0264	Ig heavy chain V r
20	63	84.0	214	2 S68212	Ig kappa chain V r
21	60	80.0	133	2 PS0023	Ig kappa chain (Ma
22	59	78.7	113	2 PT0409	Ig kappa chain pre
23	57	76.0	104	2 PH1053	Ig light chain V r
24	57	76.0	113	2 JC2270	Ig light chain V r
25	57	76.0	135	2 S38807	PL7-6 antibody lig
26	56	74.7	105	2 C30535	Ig light chain V-J
27	56	74.7	107	2 F30535	Ig kappa chain V r
28	56	74.7	107	2 D30535	Ig kappa chain V r
29	56	74.7	107	2 G30535	Ig kappa chain V r

30	56	74.7	108	2 E30535	Ig kappa chain V r
31	56	74.7	112	2 F30538	Ig kappa chain V r
32	56	74.7	112	2 E30538	Ig kappa chain V r
33	56	74.7	113	2 PL0263	Ig kappa chain V r
34	56	74.7	132	2 S46373	Ig kappa chain V-J
35	55	73.3	112	2 S09970	Ig kappa chain V-J
36	55	73.3	138	2 S26040	Ig kappa chain pre
37	54	72.0	112	2 S41393	Ig kappa chain V r
38	54	72.0	118	2 PT0356	Ig kappa chain V r
39	53	70.7	113	2 A49260	antitumor monoclon
40	53	70.7	134	2 PC1214	Ig kappa chain pre
41	52	69.3	109	2 S26336	Ig light chain V r
42	51	68.0	101	2 S26337	Ig light chain V r
43	51	68.0	103	2 PH1054	Ig light chain V r
44	51	68.0	111	2 G30502	Ig kappa chain V r
45	50	66.7	92	2 S37532	Ig kappa chain V r

ALIGNMENTS

RESULT 1  
PH1048  
Ig light chain V region (clone 165.49) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996  
C;Accession: PH1048  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1048  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-81 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin

Query Match 96.0%; Score 72; DB 2; Length 81;  
Best Local Similarity 93.8%; Pred. No. 5.9e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRRKNYL 16  
Db 3 KSSQSLSSRRKNYL 18

RESULT 2  
PH1046  
Ig light chain V region (clone 202.9) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1046  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1046  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-101 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 101;  
Best Local Similarity 93.8%; Pred. No. 7.4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRRKNYL 16

Db 24 KSSQSLNSRTRKNYL 39

RESULT 3

PH1047

Ig light chain V region (clones 165.45 and 163-cl) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1047; PH1049

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1047

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-103 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F,16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 103;  
Best Local Similarity 93.8%; Pred. No. 7.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16

Db 24 KSSQSLNSRTRKNYL 39

RESULT 4

S43103

Ig kappa chain V-J region (4B1 VL) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-May-2001

C/Accession: S43103

R/Gilbert, D.; Brard, F.; Margartite, C.; Delpech, A.; Tron, F.

submitted to the EMBL Data library, March 1994

A/Description: An Idiotypic D23-bearing polyspecific, murine anti-DNA monoclonal antibody

A/Reference number: S42484

A/Accession: S43103

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-112 <GIL>

A/Cross-references: EMBL:Z31353; NID:g467574; PIDN:CAA83231.1; PID:g467575

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F,16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 8.2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16

Db 24 KSSQSLNSRTRKNYL 39

RESULT 5

PT0408

Ig light chain V region (S107/VH11 group 1-6) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PT0408

R/Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A/Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A/Reference number: PT0376; MUID:91147903; PMID:1900082

A/Accession: PT0408

A/Molecule type: DNA

A/Residues: 1-113 <BEH>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin  
F,16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 113;  
Best Local Similarity 93.8%; Pred. No. 8.3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16

Db 24 KSSQSLNSRTRKNYL 39

RESULT 6

PT0407

Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PT0407

R/Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A/Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodie

A/Reference number: PT0376; MUID:91147903; PMID:1900082

A/Accession: PT0407

A/Molecule type: DNA

A/Residues: 1-113 <BEH>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F,16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 113;  
Best Local Similarity 93.8%; Pred. No. 8.3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16

Db 24 KSSQSLNSRTRKNYL 39

RESULT 7

G33932

Ig kappa chain precursor V region (D23) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000

C/Accession: G33932

R/Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A/Title: Two murine natural polyclonal autoantibodies are encoded by nonmutated germ-l

A/Reference number: A33932; MUID:89282823; PMID:2499887

A/Accession: G33932

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-120 <BAC>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F,36-116/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 120;  
Best Local Similarity 93.8%; Pred. No. 8.8e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16

Db 44 KSSQSLNSRTRKNYL 59

RESULT 8

PH1050

Ig light chain V region (clone 111-cl) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1050

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1050	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-103 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 103;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 9	
PH1101	
Ig light chain V region (clone 111.19) - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000	
C;Accession: PH1101	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1101	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-104 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 104;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 10	
PH1102	
Ig light chain V region (clone 111.61) - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000	
C;Accession: PH1102	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1102	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-104 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology.	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 104;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 11	
PH1103	
Ig light chain V region (clone 111.109) - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000	
C;Accession: PH1103	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1103	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-104 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 104;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 12	
PH1104	
Ig light chain V region (clone 111.100) - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000	
C;Accession: PH1104	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1104	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-104 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 104;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 13	
PL0265	
Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)	
C;Species: Mus musculus (house mouse)	
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000	
C;Accession: PL0265	
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A	
J. Exp. Med. 171, 265-297, 1990	
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic	
A;Reference number: PL0231; MUID:90111618; PMID:2104919	
A;Accession: PL0265	
A;Molecule type: mRNA	
A;Residues: 1-112 <SHL>	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	

Db 24 KSSQSLKSRTTRKNYL 39	
RESULT 11	
PH1103	
Ig light chain V region (clone 111.109) - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000	
C;Accession: PH1103	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1103	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-104 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 104;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 12	
PH1104	
Ig light chain V region (clone 111.100) - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000	
C;Accession: PH1104	
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.	
J. Exp. Med. 176, 761-779, 1992	
A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c	
A;Reference number: PH0971; MUID:92381444; PMID:1512540	
A;Accession: PH1104	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-104 <TIL>	
A;Experimental source: B cell, strain [NZB x NZW]F1	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: immunoglobulin	
F;16-96/Domain: immunoglobulin homology <IMM>	
QY	1 KSSQSLSSRTRKNYL 16
Db	24 KSSQSLKSRTTRKNYL 39
Query Match 94.7%; Score 71; DB 2; Length 104;	
Best Local Similarity 93.8%; Pred. No. 1.2e-05;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 13	
PL0265	
Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)	
C;Species: Mus musculus (house mouse)	
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000	
C;Accession: PL0265	
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A	
J. Exp. Med. 171, 265-297, 1990	
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic	
A;Reference number: PL0231; MUID:90111618; PMID:2104919	
A;Accession: PL0265	
A;Molecule type: mRNA	
A;Residues: 1-112 <SHL>	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	

Search completed: March 1, 2005, 17:44:46  
Job time : 22.6615 secs

C;Keywords: heterotetramer; immunoglobulin  
F;1-23/Region: framework 1  
F;16-96/Domain: immunoglobulin homology <IMM>  
F;24-40/Region: complementarity-determining 1  
F;41-55/Region: framework 2  
F;56-62/Region: complementarity-determining 2  
F;63-94/Region: framework 3  
F;95-102/Region: complementarity-determining 3  
F;103-112/Region: framework 4

Query Match 90.7%; Score 68; DB 2; Length 112;  
Best Local Similarity 87.5%; Pred. No. 4.4e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||:|||||  
Db 24 KSSQSLFNSRTRKNYL 39

RESULT 14

PH1051  
Ig light chain V region (clone 165.3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1051  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1051  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-103 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 67; DB 2; Length 103;  
Best Local Similarity 87.5%; Pred. No. 6.2e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||:|||||  
Db 24 KSSQSLNRRTRKNYL 39

RESULT 15

PH1052  
Ig light chain V region (clone 165.5) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1052  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1052  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-103 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 67; DB 2; Length 103;  
Best Local Similarity 87.5%; Pred. No. 6.2e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKNYL 16  
|||:|||||  
Db 24 KSMQSLNSRTRKNYL 39



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 103.631 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRTRKNYL 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	84.0	255	2 Q6KB05	Q6kb05 mus musculu
2	50	66.7	121	1 KV40_HUMAN	P06312 homo sapien
3	50	66.7	133	1 KV4B_HUMAN	P06313 homo sapien
4	50	66.7	134	1 KV4C_HUMAN	P06314 homo sapien
5	49	65.3	114	1 KV4A_HUMAN	P01625 homo sapien
6	47	62.7	109	1 KV4D_HUMAN	P83593 homo sapien
7	46	61.3	687	2 Q49728	O49728 arabidopsis
8	44	58.7	396	1 AAT_ECOLI	P00509 escherichia
9	44	58.7	396	1 AAT_SALTI	Q56114 salmoneilla
10	44	58.7	396	1 AAT_SALTY	P58661 salmoneilla
11	44	58.7	396	2 Q7N625	Q7n625 photorhabdu
12	44	58.7	396	2 Q8FJ99	O8fj99 escherichia
13	44	58.7	396	2 Q83LN4	Q83ln4 shigella fl
14	44	58.7	396	2 Q8XDF3	Q8xdf3 escherichia
15	42	56.0	333	2 Q6MCL8	Q6mcl8 parachlamyd
16	42	56.0	358	2 Q8EJG4	Q8ejg4 shewanella
17	42	56.0	572	2 Q6IFZ6	Q6ifz6 mus musculu
18	41	54.7	216	2 Q9CGK7	Q9cgk7 lactococcus
19	41	54.7	519	2 Q6IG01	Q6ig01 rattus norv
20	41	54.7	560	2 Q8HHY2	Q8hhy2 helianthus
21	41	54.7	624	2 Q93Y37	Q93y37 arabidopsis
22	41	54.7	792	2 Q6CXCl	Q6cxc1 kluyveromyc
23	40	53.3	106	2 Q82561	Q82561 elaeagnus u
24	40	53.3	336	2 Q16329	O16329 caenorhabdi
25	40	53.3	336	2 Q16330	O16330 caenorhabdi
26	40	53.3	396	2 Q9RNA0	Q9rna0 aeromonas h
27	40	53.3	397	2 Q9JVS3	Q9jvs3 neisseria m
28	40	53.3	397	2 Q9K0P5	Q9k0p5 neisseria m
29	40	53.3	398	2 Q7QMD9	Q7qmd9 anopheles g
30	40	53.3	433	2 Q6LYX4	Q6lyx4 methanococc
31	40	53.3	656	2 Q7MGG8	Q7mgg8 vibrio vuln

32	40	53.3	656	2 Q8D4W4	Q8d4w4 vibrio vuln
33	40	53.3	657	2 Q72P01	Q72p01 leptospira
34	40	53.3	657	2 Q8F7G0	Q8f7g0 leptospira
35	40	53.3	1212	2 Q7X5Q3	Q7x5q3 anaplasma p
36	40	53.3	1216	2 Q7X5P8	Q7x5p8 anaplasma p
37	40	53.3	1216	2 Q7X5Q0	Q7x5q0 anaplasma p
38	40	53.3	1216	2 Q7X5Q4	Q7x5q4 anaplasma p
39	40	53.3	1216	2 Q7X5Q7	Q7x5q7 anaplasma p
40	40	53.3	1216	2 Q7X5Q8	Q7x5q8 anaplasma p
41	40	53.3	1216	2 Q7X5Q9	Q7x5q9 anaplasma p
42	40	53.3	1216	2 Q7X5R0	Q7x5r0 anaplasma p
43	40	53.3	3007	2 Q14215	Q14215 homo sapien
44	40	53.3	6669	1 NEBU_HUMAN	P20929 homo sapien
45	39	52.0	47	1 RL34_WIGBR	Q8d3i7 wigleswort

ALIGNMENTS

RESULT 1					
ID	Q6KB05	PRELIMINARY;	PRT;	255 AA.	
AC	Q6KB05;				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, last annotation update)				
DE	ScFv B8E5 protein (Fragment).				
GN	Name=scFv B8E5;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa;				Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria;				Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Balb/c;				
RA	Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,				
RA	Briand J.P., Hoebeke J.;				
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ746180; CAG84081.1; -.				
DR	HSSP; P01837; IKCR.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-1like.				
DR	InterPro; IPR003596; Ig_v.				
DR	SMART; SM00409; IG; 2.				
DR	SMART; SM00406; IGv; 2.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE	255 AA;	27445 MW;	B68BD38395DF713B CRC64;	
Query Match					
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Matches 13; Conservativity 2; Mismatches 1; Indels 0; Gaps 0;					
QY	1 KSSQSLSSRTRKNYL 16				
Db	160 KSSQSLSSRTRKNYL 175				
RESULT 2					
ID	KV40_HUMAN	STANDARD;	PRT;	121 AA.	
AC	P06312;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, last sequence update)				
DT	05-JUL-2004 (Rel. 44, last annotation update)				
DE	Ig kappa chain V-IV region precursor (Fragment).				
GN	Name=IGKV4-1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa;				Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria;				Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

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RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -I- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
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CC -----
DR EMBL; Z00023; CAA77318.1; -.
DR PIR; A01902; KAHU.
DR HSSP; P01625; ILVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 >121 Ig kappa chain V-IV region.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4180D33974 CRC64;

Query Match
Best Local Similarity 66.7%; Score 50; DB 1; Length 121;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16
Db 44 KSSQSVLYSSNNKNYL 59

RESULT 3
KV4B_HUMAN STANDARD; PRT; 133 AA.
ID P06313;
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
DR EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; KAHUJI.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20 Ig kappa chain V-IV region JI.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DOMAIN 115 122 Framework-4.
FT DOMAIN 123 132 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match
Best Local Similarity 66.7%; Score 50; DB 1; Length 133;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16
Db 44 KSSQSVLYSSNNKNYL 59

RESULT 4
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X02990; CAA26733.1; -.

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DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DOMAIN 115 121 Framework-3.
FT DOMAIN 122 133 Complementarity-determining-4.
FT DISULFID 43 114 By similarity.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 66.7%; Score 50; DB 1; Length 134;
Best Local Similarity 68.8%; Pred. No. 0.41;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKKNYL 16
Db 44 KSSQSILYSSDNKNYL 59

RESULT 5
KV4A_HUMAN STANDARD; PRT; 114 AA.
ID KV4A_HUMAN
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-IV region len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; Pubmed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1EEQ; X-ray; A/B=1-114.
DR PDB; 1EEU; X-ray; A/B=1-114.
DR PDB; 1EFQ; X-ray; A=1-114.
DR PDB; 1EK3; X-ray; A/B=1-114.
DR PDB; 1LVE; X-ray; @=1-114.
DR PDB; 3LVE; X-ray; @=1-114.
DR PDB; 5LVE; X-ray; A=1-114.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
```

```
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 40 Complementarity-determining-1.
FT DOMAIN 41 55 Complementarity-determining-2.
FT DOMAIN 56 62 Complementarity-determining-3.
FT DOMAIN 63 94 Framework-3.
FT DOMAIN 95 101 Complementarity-determining-4.
FT DOMAIN 102 113 Framework-4.
FT DISULFID 23 94 By similarity.
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 32 35
FT STRAND 36 37
FT STRAND 39 44
FT STRAND 46 47
FT STRAND 51 55
FT STRAND 56 58
FT STRAND 59 60
FT STRAND 62 63
FT STRAND 66 67
FT STRAND 68 73
FT STRAND 74 75
FT STRAND 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 65.3%; Score 49; DB 1; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.52;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTRKKNYL 16
Db 24 KSSQSVLYSSNSKNYL 39

RESULT 6
KV4D_HUMAN STANDARD; PRT; 109 AA.
ID KV4D_HUMAN
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RP TISSUE=Abdominal adipose tissue;
RC MEDLINE=98249779; Pubmed=9588180; DOI=10.1006/bhrc.1998.8515;
RX Olsen K.E., Sletten K., Westermarck P.;
RA "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -1- FUNCTION: May play an important role in fibrillogenesis.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 40 Complementarity-determining-1.
FT DOMAIN 41 55 Framework-2.
FT DOMAIN 56 62 Complementarity-determining-2.
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FT  DOMAIN      63      94      Framework-3.
FT  DOMAIN      95      101     Complementarity-determining-3.
FT  DOMAIN      102     109     Framework-4.
FT  DISULFID     23      94      By similarity.
FT  UNSURE       23      23
FT  UNSURE       94      94
FT  NON TER      109     109
SQ  SEQUENCE     109 AA; 12060 MW; 0C4F31E11E12A0B CRC64;

Query Match
Best Local Similarity 62.7%; Score 47; DB 1; Length 109;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY  1 KSSQSLSSRTKKNYL 16
    :|||:|:|
Db  24 RSSQSVLYSSNNKNYL 39

RESULT 7
ID  049728      PRELIMINARY;      PRT;      687 AA.
AC  049728;
DT  01-JUN-1998 (TRENBLREL. 06, Created)
DT  01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT  05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE  Receptor serine/threonine kinase-like protein.
GN  Name=T9A21.100; Synonyms=AT4g18250;
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX  NCBI_TaxID=3702;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA  Mayer K.F.X., Lemcke K., Schueller C.;
RL  Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RA  EU Arabidopsis sequencing project;
RL  Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RA  Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RA  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN  [4]
RP  SEQUENCE FROM N.A.
RA  EU Arabidopsis sequencing project;
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR  EMBL; AL021713; CAA16797.1; -.
DR  EMBL; AL161548; CAB78827.1; -.
DR  PIR; T04927; T04927.
DR  HSSP; P02883; IRCW.
DR  GO; GO:0005524; F:ATP binding; IEA.
DR  GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0016740; F:transferase activity; IEA.
DR  GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR  InterPro; IPR011009; Kinase like.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR001938; Thumatin.
DR  Pfam; PF00314; Thumatin; 2.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  ProDom; PD001321; Thumatin; 2.
DR  SMART; SM00205; THN; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR  PROSITE; PS00316; THAUMATIN; UNKNOWN_1.
KW  ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
    Transferase.

```

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SQ  SEQUENCE     687 AA;  77096 MW;  3D2E557112AF2C84 CRC64;

Query Match
Best Local Similarity 61.3%; Score 46; DB 2; Length 687;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  2 SSQSLSSRTKKNY 15
    |:|||||:|
Db  667 STQSLERKTRSNY 680

RESULT 8
AAT_ECOLI
ID  AAT_ECOLI      STANDARD;      PRT;      396 AA.
AC  P00509;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  25-JAN-2005 (Rel. 46, Last annotation update)
DE  Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPART).
GN  Name=aspC; OrderedlocusNames=b0928;
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85289110; PubMed=3897210;
RA  Kuramitsu S., Okuno S., Ogawa T., Ogawa H., Kagamiyama H.;
RT  "Aspartate aminotransferase of Escherichia coli: nucleotide sequence
    of the aspC gene.";
RL  J. Biochem. 97:1259-1262 (1985).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=8624211; PubMed=3521591;
RA  Fotheringham I.G., Dacey S.A., Taylor P.P., Smith T.J., Hunter M.G.,
RA  Finlay M.E., Primrose S.B., Parker D.M., Edwards R.M.;
RT  "The cloning and sequence analysis of the aspC and tyrB genes from
    Escherichia coli K12. Comparison of the primary structures of the
    aspartate aminotransferase and aromatic aminotransferase of E. coli
    with those of the pig aspartate aminotransferase isoenzymes.";
RL  Biochem. J. 234:593-604 (1986).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=K12 / MG1655;
RX  MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA  Mau B., Shao Y.;
RT  "The complete genome sequence of Escherichia coli K-12.";
RL  Science 277:1453-1474 (1997).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=K12;
RX  MEDLINE=97061202; PubMed=8905232;
RA  Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA  Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA  Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA  Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA  Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA  Yano M., Horiuchi T.;
RT  "A 718-kb DNA sequence of the Escherichia coli K-12 genome
    corresponding to the 12.7-28.0 min region on the linkage map.";
RL  DNA Res. 3:137-155 (1996).
RN  [5]
RP  SEQUENCE.
RX  MEDLINE=84256832; PubMed=6378205;
RA  Kondo K., Wakabayashi S., Yagi T., Kagamiyama H.;
RT  "The complete amino acid sequence of aspartate aminotransferase from
    Escherichia coli: sequence comparison with pig isoenzymes.";
RL  Biochem. Biophys. Res. Commun. 122:62-67 (1984).
RN  [6]
RP  SEQUENCE.

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RX MEDLINE=87250482; PubMed=3298240;  
RA Kondo K., Wakabayashi S., Kagamiyama H.;  
RT "Structural studies on aspartate aminotransferase from Escherichia  
RT coli. Covalent structure."  
RL J. Biol. Chem. 262:8648-8659(1987).  
RN [7]  
RN SEQUENCE OF 1-12.  
RC STRAIN=K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded  
RT in the genome of Escherichia coli K-12."  
RL Electrophoresis 18:1259-1313(1997).  
RN [8]  
RN MUTAGENESIS OF TYR-65.  
RP MEDLINE=91329346; PubMed=1868057;  
RX Inoue K., Kuramitsu S., Okamoto A., Hirotsu K., Higuchi T.,  
RA Kagamiyama H.;  
RT "Site-directed mutagenesis of Escherichia coli aspartate  
RT aminotransferase: role of Tyr70 in the catalytic processes."  
RL Biochemistry 30:7796-7801(1991).  
RN [9]  
RN MUTAGENESIS OF HIS-133.  
RX MEDLINE=91177849; PubMed=2007566;  
RA Yano T., Kuramitsu S., Tanase S., Morino Y., Hiromi K., Kagamiyama H.;  
RT "The role of His143 in the catalytic mechanism of Escherichia coli  
RT aspartate aminotransferase."  
RL J. Biol. Chem. 266:6079-6085(1991).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MUTANT ALA-246.  
RX MEDLINE=90105323; PubMed=2513875;  
RA Smith D.L., Almo S.C., Toney M.D., Ringe D.;  
RT "2.8-A-resolution crystal structure of an active-site mutant of  
RT aspartate aminotransferase from Escherichia coli."  
RL Biochemistry 28:8161-8177(1989).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND MUTAGENESIS OF ARG-374.  
RX MEDLINE=91129283; PubMed=1993208;  
RA Danishefsky A.T., Ommeter J.J., Petsko G.A., Ringe D.;  
RT "Activity and structure of the active-site mutants R386Y and R386F of  
RT Escherichia coli aspartate aminotransferase."  
RL Biochemistry 30:1980-1985(1991).  
RN [12]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF MUTANT.  
RX MEDLINE=99107891; PubMed=9891001; DOI=10.1074/jbc.274.4.2344;  
RA Oue S., Okamoto A., Yano T., Kagamiyama H.;  
RT "Redesigning the substrate specificity of an enzyme by cumulative  
RT effects of the mutations of non-active site residues."  
RL J. Biol. Chem. 274:2344-2349(1999).  
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
CC L-glutamate.  
CC -1- COFACTOR: Pyridoxal phosphate.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent  
CC aminotransferase family.  
CC -----  
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CC -----  
DR EMBL; X03629; CAA27279.1; -  
DR EMBL; X05904; CAA29333.1; -  
DR EMBL; U00096; AAC74014.1; -  
DR EMBL; D90730; BAA35674.1; -  
DR EMBL; D90731; BAA35680.1; -  
DR PIR; A00598; XNECD.  
DR PDB; 1AAM; X-ray; @=1-396.  
DR PDB; 1AAW; X-ray; @=1-396.

DR PDB; 1AHE; X-ray; A/B=1-396.  
DR PDB; 1AHF; X-ray; A/B=1-396.  
DR PDB; 1AHG; X-ray; A/B=1-396.  
DR PDB; 1AHX; X-ray; A/B=1-396.  
DR PDB; 1AHY; X-ray; A/B=1-396.  
DR PDB; 1AIA; X-ray; A/B=1-396.  
DR PDB; 1AIB; X-ray; A/B=1-396.  
DR PDB; 1AIC; X-ray; A/B=1-396.  
DR PDB; 1AMQ; X-ray; @=1-396.  
DR PDB; 1AMR; X-ray; @=1-396.  
DR PDB; 1AMS; X-ray; @=1-396.  
DR PDB; 1ARG; X-ray; A/B=1-396.  
DR PDB; 1ARH; X-ray; A/B=1-396.  
DR PDB; 1ARI; X-ray; A/B=1-396.  
DR PDB; 1ARS; X-ray; @=1-396.  
DR PDB; 1ART; X-ray; @=1-396.  
DR PDB; 1ASA; X-ray; @=1-396.  
DR PDB; 1ASB; X-ray; @=1-396.  
DR PDB; 1ASC; X-ray; @=1-396.  
DR PDB; 1ASD; X-ray; @=1-396.  
DR PDB; 1ASE; X-ray; @=1-396.  
DR PDB; 1ASF; X-ray; @=1-396.  
DR PDB; 1ASG; X-ray; @=1-396.  
DR PDB; 1ASL; X-ray; A/B=1-396.  
DR PDB; 1ASM; X-ray; A/B=1-396.  
DR PDB; 1ASN; X-ray; A/B=1-396.  
DR PDB; 1B4X; X-ray; A=1-396.  
DR PDB; 1BQA; X-ray; A/B=1-396.  
DR PDB; 1BQD; X-ray; A/B=1-396.  
DR PDB; 1C9C; X-ray; A=1-396.  
DR PDB; 1C06; X-ray; A=1-396.  
DR PDB; 1C07; X-ray; A=1-396.  
DR PDB; 1C08; X-ray; A=1-396.  
DR PDB; 1CZC; X-ray; A=1-396.  
DR PDB; 1CZE; X-ray; A=1-396.  
DR PDB; 1G4V; X-ray; A=1-396.  
DR PDB; 1G4X; X-ray; A=1-396.  
DR PDB; 1G7W; X-ray; A=1-396.  
DR PDB; 1G7X; X-ray; A=1-396.  
DR PDB; 1IX6; X-ray; A=1-396.  
DR PDB; 1IX7; X-ray; A=1-396.  
DR PDB; 1IX8; X-ray; A=1-396.  
DR PDB; 1QIR; X-ray; A=1-396.  
DR PDB; 1QIS; X-ray; A=1-396.  
DR PDB; 1QIT; X-ray; A=1-396.  
DR PDB; 1SPA; X-ray; @=1-396.  
DR PDB; 1YOO; X-ray; @=1-396.  
DR PDB; 2AAT; X-ray; @=1-396.  
DR PDB; 3AAT; X-ray; @=1-396.  
DR PDB; 5EAA; X-ray; A=1-396.  
DR SWISS-2DPAGE; P00509; COL1.  
DR ECO2DBASE; F039.6; 6TH EDITION.  
DR ECO2DBASE; F039.7; 6TH EDITION.  
DR ECHOBASE; EB0094; -.  
DR EcoGene; EG10096; aspC.  
DR InterPro; IPR004839; Aminotrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; Nhltransf\_1\_BS.  
DR Pfam; PF00155; Aminotran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW 3D-structure; Aminotransferase; Complete proteome;  
KW Direct protein sequencing; Pyridoxal phosphate; Transferrase.  
FT BINDING 246 246  
FT ACT SITE 374 374  
FT MUTAGEN 133 133

H->A: Slight increase in maximum velocity;  
of the overall transamination reaction

Query Match 58.7%; Score 44; DB 1; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRTRKNYL 16



Db 51 KAEQYLLNETTKNYL 66

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RESULT 9
AAT_SALTY
ID AAT_SALTY STANDARD; PRT; 396 AA.
AC Q56114;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (AspAT).
GN Name=aspC; OrderedLocuNames=STY1000, t1936;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leacher S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RL enterica serovar Typhi CT18.";
RN Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
RN [3]
RP SEQUENCE OF 1-74 FROM N.A.
RC STRAIN=IMSS-1;
RA Fernandez-Mora M., Calva E.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
CC L-glutamate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent
CC aminotransferase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL627268; CAD05398.1; -.
DR EMBL; AE016840; AA069551.1; -.
DR EMBL; X89757; CAA61906.1; -.
DR HSSP; P00509; 1ART.
DR InterPro; IPR004839; Aminotrans_I/II.
DR InterPro; IPR000796; Asp_trans.
DR InterPro; IPR004838; NHTransf_1_BS.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PRINTS; PR00799; TRANSAMINASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
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KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.  
FT BINDING 246 246 Pyridoxal phosphate (By similarity).  
FT ACT\_SITE 374 374  
SQ SEQUENCE 396 AA; 43507 MW; 974C1585438D02FB CRC64;

Query Match 58.7%; Score 44; DB 1; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTKKNYL 16  
Db 51 KAEQYLLNETTKNYL 66

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RESULT 10
AAT_SALTY
ID AAT_SALTY STANDARD; PRT; 396 AA.
AC P58661;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (AspAT).
GN Name=aspC; OrderedLocuNames=STW0998;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL LT2.";
RN Nature 413:852-856(2001).
RC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
CC L-glutamate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent
CC aminotransferase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE008743; AAL19932.1; -.
DR HSSP; P00509; 1ART.
DR StyGene; SG7777?; aspC.
DR InterPro; IPR004839; Aminotrans_I/II.
DR InterPro; IPR000796; Asp_trans.
DR InterPro; IPR004838; NHTransf_1_BS.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PRINTS; PR00799; TRANSAMINASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
FT BINDING 246 246 Pyridoxal phosphate (By similarity).
FT ACT_SITE 374 374
SQ SEQUENCE 396 AA; 43521 MW; 960940D0148D02FB CRC64;
```

Query Match 58.7%; Score 44; DB 1; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| : | | | : | | | |  
Db 51 KAEQYLLENETTKNYL 66

RESULT 11  
Q7N625 PRELIMINARY; PRT; 396 AA.

ID Q7N625; PRELIMINARY; PRT; 396 AA.  
AC Q7N625;  
DT 01-MAR-2004 (TReMBLrel. 26, Created)  
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Aspartate aminotransferase (Transaminase A).  
GN Name=aspc; OrderedLocuNames=plu1750;  
OS Photorhabdus luminescens (subsp. laumondii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Photorhabdus.  
OX NCBI\_TaxID=141679;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=T01;  
RX MEDLINE=22957627; PubMed=14528314;  
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,  
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,  
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,  
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;  
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus  
RT luminescens.";  
RT Nat. Biotechnol. 21:1307-1313(2003).  
RL EMBL; BX571864; CAE14043.1; -.  
DR HSSP; P00509; IART.  
DR Photolyst; plu1750; -.  
DR GO; GO:0008483; F:transaminase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR InterPro; IPR004839; AminoTrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; NHtransf\_1\_BS.  
DR Pfam; PF00155; AminoTran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW AminoTransferase; Complete proteome; Transferase.  
SQ SEQUENCE 396 AA; 43575 MW; 7EC3E64A6DBC6C26 CRC64;

Query Match 58.7%; Score 44; DB 2; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| : | | | : | | | |  
Db 51 KAEQYLLENETTKNYL 66

RESULT 12  
Q8FJ99 PRELIMINARY; PRT; 396 AA.

ID Q8FJ99; PRELIMINARY; PRT; 396 AA.  
AC Q8FJ99;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Aspartate aminotransferase (EC 2.6.1.1).  
GN Name=aspc; OrderedLocuNames=c1070;  
OS Escherichia coli O6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=217992;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;  
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

RA Raske D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
RT of uropathogenic Escherichia coli.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
DR EMBL; AE016758; AAN79538.1; -.  
DR HSSP; P00509; IART.  
DR GO; GO:0004069; F:aspartate transaminase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR InterPro; IPR004839; AminoTrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; NHtransf\_1\_BS.  
DR Pfam; PF00155; AminoTran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW AminoTransferase; Complete proteome; Transferase.  
SQ SEQUENCE 396 AA; 43568 MW; 9F4A6ECB413FC679 CRC64;

Query Match 58.7%; Score 44; DB 2; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
| : | | | : | | | |  
Db 51 KAEQYLLENETTKNYL 66

RESULT 13  
Q83LN4 PRELIMINARY; PRT; 396 AA.

ID Q83LN4; PRELIMINARY; PRT; 396 AA.  
AC Q83LN4; Q7C286;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Aspartate aminotransferase.  
GN Name=aspc; OrderedLocuNames=S0989, SF0925;  
OS Shigella flexneri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Shigella.  
OX NCBI\_TaxID=623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=301 / Serotype 2a;  
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;  
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
RA Yu J.;  
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity  
RT through comparison with genomes of Escherichia coli K12 and O157.";  
RL Nucleic Acids Res. 30:4432-4441(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2457T;  
RX MEDLINE=22590274; PubMed=12704152;  
RX DOI=10.1128/IAI.71.5.2775-2786.2003;  
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,  
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,  
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,  
RA Schwartz D.C., Blattner F.R.;  
RT "Complete genome sequence and comparative genomics of Shigella  
RT flexneri serotype 2a|strain 2457T.";  
RL Infect. Immun. 71:2775-2786(2003).  
DR EMBL; AE015122; AAN42554.1; -.  
DR EMBL; AE016981; AAP16440.1; -.  
DR HSSP; P00509; IART.  
DR GO; GO:0008483; F:transaminase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.

DR InterPro; IPR004839; AminoTrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; Nhltransf\_1\_BS.  
DR Pfam; PF00155; AminoTran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW AminoTransferase; Transferase; Complete proteome.  
SQ SEQUENCE 396 AA; 43617 MW; 621C1FB9FBA4DD5A CRC64;

Query Match 58.7%; Score 44; DB 2; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNYL 16  
|:| |:| |:| |:|  
Db 51 KAEQYLLENETTKNYL 66

RESULT 14  
Q8XDF3 PRELIMINARY; PRT; 396 AA.  
ID Q8XDF3; Q7AG50;  
AC Q8XDF3; Q7AG50;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Aspartate aminotransferase.  
GN Name=aspC; OrderedLocustNames=ECs1011, 21275;  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=83334;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;  
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;  
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
RL Nature 409:529-533(2001).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22(2001).  
DR EMBL; AE005282; AAG55413.1; -.  
DR EMBL; AP002553; BAB34434.1; -.  
DR PIR; A85619; A85619.  
DR PIR; C90755; C90755.  
DR HSSP; P00509; IART.  
DR GO; GO:0008483; F:transaminase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR GO; GO:0009058; P:biosynthesis; IEA.  
DR InterPro; IPR004839; AminoTrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; Nhltransf\_1\_BS.  
DR Pfam; PF00155; AminoTran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW AminoTransferase; Transferase; Complete proteome.  
SQ SEQUENCE 396 AA; 43645 MW; 81C2063CE24DFF08 CRC64;

Query Match 58.7%; Score 44; DB 2; Length 396;

Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 KSSQSLSSRTRKNYL 16  
|:| |:| |:| |:|  
Db 51 KAEQYLLENETTKNYL 66

RESULT 15  
Q6MCL8 PRELIMINARY; PRT; 333 AA.  
ID Q6MCL8;  
AC Q6MCL8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=pc0957;  
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).  
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.  
OX NCBI\_TaxID=264201;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
RA Rattei T., Mewes H.-W., Wagner M.;  
RT "Genome sequence of an amoeba symbiont and its use for reconstructing  
the evolutionary history of chlamydiae.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX908798; CAF23681.1; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 333 AA; 39257 MW; 6C88A8E88C85D816 CRC64;

Query Match 56.0%; Score 42; DB 2; Length 333;  
Best Local Similarity 53.3%; Pred. No. 37;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTRKNY 15  
|:| |:| |:| |:|  
Db 16 EDKSSLLTNRIRKNY 30

Search completed: March 1, 2005, 17:43:17  
Job time : 105.631 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: March 1, 2005, 17:16:08 ; Search time 52.3385 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	100.0	7	2	AAR30157	Aar30157 MAb GAH v
2	38	100.0	7	2	AAR57966	Aar57966 MAB NFS2
3	38	100.0	7	2	AAR50317	Aar50317 MAB NFS2
4	38	100.0	7	2	AAR57964	Aar57964 MAB NFS2
5	38	100.0	7	2	AAV08713	Aay08713 Human mil
6	38	100.0	7	3	AAV95234	Aay95234 Human mon
7	38	100.0	7	3	AAV32227	Aay32227 G-CSF ago
8	38	100.0	7	3	AAB07952	Aab07952 CDR2 sequ
9	38	100.0	7	5	AAU81257	Aau81257 Human trk
10	38	100.0	7	5	ABP62361	Abp62361 Human imm
11	38	100.0	7	5	AAE29275	Aae29275 Anti-ClfA
12	38	100.0	7	5	ABG68854	Abg68854 CDR2 VL p
13	38	100.0	7	5	AAU70347	Aau70347 Mouse Kap
14	38	100.0	7	5	AAU70335	Aau70335 Human Kap
15	38	100.0	7	6	AAE34369	Aae34369 Escherich
16	38	100.0	7	6	ABP98689	Abp98689 Human GAH
17	38	100.0	7	6	ABP98681	Abp98681 Human GAH
18	38	100.0	7	6	ABG71653	Abg71653 CDR2 of H
19	38	100.0	7	6	AAE38110	Aae38110 Human COU
20	38	100.0	7	7	ABO33872	AbO33872 Anti-GPI-
21	38	100.0	7	7	ABO33869	AbO33869 Anti-GPI-
22	38	100.0	7	7	ADC97709	Adc97709 Mouse mon
23	38	100.0	7	7	ADG43867	Adg43867 Human pep
24	38	100.0	7	8	ADL23027	Adl23027 Myelin as
25	38	100.0	7	8	ADO32089	Ado32089 Mouse ant

26	38	100.0	7	8	ADO58066	Ado58066 S2 cell d
27	38	100.0	7	8	ADP47268	Adp47268 Human pho
28	38	100.0	7	8	ADP47250	Adp47250 Human pho
29	38	100.0	7	8	ADP47241	Adp47241 Human pho
30	38	100.0	7	8	ADP47271	Adp47271 Human pho
31	38	100.0	7	8	ADP47286	Adp47286 Human pho
32	38	100.0	7	8	ADQ28264	Adq28264 Method of
33	38	100.0	7	8	ADS88787	Ads88787 Light cha
34	38	100.0	12	8	ADO32134	Ado32134 Mouse ant
35	38	100.0	15	5	ABG68859	Abg68859 CDR2 sequ
36	38	100.0	17	8	ADR38445	Adr38445 Human N-t
37	38	100.0	82	2	AAW62807	Aaw62807 Amino aci
38	38	100.0	84	2	AAW14491	Aaw14491 Monoclonal
39	38	100.0	84	2	AAV56669	Aay56669 Partial p
40	38	100.0	94	3	ADC99827	Adc99827 Anti-huma
41	38	100.0	98	7	ADD05431	Add05431 Anti-MUC1
42	38	100.0	98	7	ADF09869	Adf09869 Anti-MUC1
43	38	100.0	98	7	ADG43869	Adg43869 Anti-MUC1
44	38	100.0	99	8	ADJ18696	Adj18696 Antibody
45	38	100.0	101	6	ABJ18696	Abj18696 Antibody

ALIGNMENTS

RESULT 1					
AAAR30157	AAAR30157	standard; protein; 7 AA.			
ID	AAAR30157;				
XX					
AC	AAAR30157;				
XX					
DT	25-MAR-2003	(revised)			
DT	06-MAY-1993	(first entry)			
XX					
DE	MAB GAH variable region of light chain.				
XX					
KW	Monoclonal antibody; hybridoma; PCR; variable region; constant region;				
KW	heavy chain; light chain.				
XX					
OS	Synthetic.				
XX					
PN	EP520499-A1.				
XX					
PD	30-DEC-1992.				
XX					
PF	26-JUN-1992;	92EP-00110841.			
XX					
PR	28-JUN-1991;	91JP-00158859.			
PR	28-JUN-1991;	91JP-00158860.			
PR	28-JUN-1991;	91JP-00158861.			
XX					
PA	(MITU ) MITSUBISHI KASEI CORP.				
XX					
PI	HOBOKAWA S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;				
XX					
DR	WPI; 1993-001328/01.				
DR	N-PSDB; AAQ33044.				
XX					
PT	Human monoclonal antibody specific for a cancer cell membrane surface				
PT	antigen - prepd. from a hybridoma obtd. by cell fusion between human				
PT	lymphocytes derived from cancer patients and mouse myeloma cells.				
XX					
PS	Claim 3; Page 30 + 23; 37pp; English.				
XX					
CC	The sequence is described is the specification as having 27 bases. A				
CC	human Mab specifically binding to a surface antigen of cancer cell				
CC	membrane comprises variable regions of the heavy and light chains having				
CC	the amino acid sequences of AAR30153-55 and AAR30156-58 respectively,				
CC	encoded by DNA sequences AAQ33040-42 and AAQ33043-45 respectively. The				
CC	antibody is obtained from a hybridoma producing human antibody GAH.				
CC	(Updated on 25-MAR-2003 to correct PN field.)				
XX					
SO	Sequence 7 AA;				



Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 2  
AAR57966 standard; protein; 7 AA.  
ID AAR57966  
XX AC AAR57966;  
XX DT 25-MAR-2003 (revised)  
DT 05-OCT-1994 (first entry)  
XX DE MAb NFS2 light chain variable region CDR2 (modified).  
XX KW Monoclonal antibody; Plasmodium falciparum; CDR;  
KW complementarity determining region; fusion protein; murine; variable;  
KW light; heavy; chain; malaria.  
XX OS Synthetic.  
XX PN WO9405690-A1.  
XX PD 17-MAR-1994.  
XX PF 08-SEP-1993; 93WO-US008435.  
XX PR 09-SEP-1992; 92US-00941654.  
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (USNA ) US SEC OF NAVY.  
PA (USSA ) US SEC OF ARMY.  
XX PI Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;  
PI Charoenvit Y, Hurle M;  
XX DR WPI; 1994-101115/12.  
DR N-PSDB; AAQ44839.  
XX PT New engineered antibodies and fusion proteins for preventing Plasmodium  
PT infection - contg. murine antibody CDR sequences, and corresp. nucleic  
PT acid, vectors and transformed cells.  
XX PS Disclosure; Page 69; 98pp; English.  
XX CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable  
CC light chain and variable heavy chain sequences derived from murine mAb  
CC NFS2 are provided. Murine mAb NFS2, its variable chain peptides, CDRs,  
CC functional fragments, Fab fragments, and analogs are useful in prodn. of  
CC fusion proteins, esp. engineered antibodies. These prods. are used to  
CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 3  
AAR50317  
ID AAR50317 standard; protein; 7 AA.

XX AC AAR50317;  
XX DT 25-MAR-2003 (revised)  
DT 05-OCT-1994 (first entry)  
XX DE MAb NFS2 light chain variable region CDR2 (modified).  
XX KW Monoclonal antibody; Plasmodium falciparum; CDR;  
KW complementarity determining region; fusion protein; murine; variable;  
KW light; heavy; chain; malaria.  
XX OS Synthetic.  
XX PN WO9405690-A1.  
XX PD 17-MAR-1994.  
XX PF 08-SEP-1993; 93WO-US008435.  
XX PR 09-SEP-1992; 92US-00941654.  
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (USNA ) US SEC OF NAVY.  
PA (USSA ) US SEC OF ARMY.  
XX PI Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;  
PI Charoenvit Y, Hurle M;  
XX DR WPI; 1994-101115/12.  
DR N-PSDB; AAQ44833.  
XX PT New engineered antibodies and fusion proteins for preventing Plasmodium  
PT infection - contg. murine antibody CDR sequences, and corresp. nucleic  
PT acid, vectors and transformed cells.  
XX PS Claim 16; Page 83; 98pp; English.  
XX CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable  
CC light chain and variable heavy chain sequences derived from murine mAb  
CC NFS2 are provided. Murine mAb NFS2, its variable chain peptides, CDRs,  
CC functional fragments, Fab fragments, and analogs are useful in prodn. of  
CC fusion proteins, esp. engineered antibodies. These prods. are used to  
CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 4  
AAR57964  
ID AAR57964 standard; protein; 7 AA.

XX AC AAR57964;  
XX DT 25-MAR-2003 (revised)  
DT 05-OCT-1994 (first entry)  
XX DE MAb NFS2 light chain variable region CDR2.

XX KW Monoclonal antibody; Plasmodium falciparum; CDR;  
KW complementarity determining region; fusion protein; murine; variable;  
KW light; heavy; chain; malaria.

OS Plasmodium falciparum.



XX WO9405690-A1.  
PN  
XX 17-MAR-1994.  
PD  
XX  
PF 08-SEP-1993; 93WO-US008435.  
XX  
PR 09-SEP-1992; 92US-00941654.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (USNA ) US SEC OF NAVY.  
PA (USSA ) US SEC OF ARMY.  
XX  
PI Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;  
PI Charoenvit Y, Hurle M;  
XX  
DR WPI; 1994-101115/12.  
DR N-PSDB; AAQ44837.  
XX  
PT New engineered antibodies and fusion proteins for preventing Plasmodium  
PT infection - contg. murine antibody CDR sequences, and corresp. nucleic  
PT acid, vectors and transformed cells.  
XX  
PS Disclosure; Page 68; 98pp; English.  
XX  
CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable  
CC light chain and variable heavy chain sequences derived from murine mAb  
CC NFS2 are provided. Murine mAb NFS2, its variable chain peptides, CDRs,  
CC functional fragments, Fab fragments, and analogs are useful in prodn. of  
CC fusion proteins, esp. engineered antibodies. These prods. are used to  
CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 5  
AA08713  
ID AAY08713 standard; protein; 7 AA.  
XX  
AC AAY08713;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human milk fat globule antigen binding fragment 5.  
XX  
KW Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;  
KW complementarity determining region; infectious disease agent antigen;  
KW cellular receptor; infectious agent; chemotherapeutic agent; vaccine;  
KW cancer; infectious disease; autoimmune disease; rheumatoid arthritis;  
KW ulcerative colitis; psoriasis; allergy; immunoassay reagent; diagnosis;  
KW veterinary medicine; antibody; immunisation; antibody; immune tolerance;  
KW human milk fat globule antigen; cryptic expression;  
KW anti-idiotypic immune response.  
XX  
OS Homo sapiens.  
XX  
PN WO925378-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 13-NOV-1998; 98WO-US024302.  
XX  
PR 14-NOV-1997; 97US-0065716P.  
PR 10-APR-1998; 98US-0081403P.  
XX

XX (EURO-) EUROCELTIQUE SA.  
PA  
XX Burch RM;  
PI  
XX  
DR WPI; 1999-357555/30.  
XX  
PT Modified immunoglobulins including engineered binding site.  
XX  
PS Claim 9; Page 76; 123pp; English.  
XX  
CC This invention describes a novel modified immunoglobulin (mig), or its  
CC fragment, that binds immunospecifically to one member (M1) of a binding  
CC pair comprises a variable domain (V) having at least one CDR  
CC (complementarity determining region) that contains a portion of the  
CC second member (M2) of the pair. This portion is not present in the  
CC natural CDR and M1 is a cancer antigen, infectious disease agent antigen,  
CC a cellular receptor for an infectious agent (provided the binding site is  
CC not NAMP or NVD) or a member of a receptor-ligand pair. mig (also  
CC related molecules containing the same V region), optionally coupled to a  
CC chemotherapeutic agent, are used in therapeutic and/or prophylactic  
CC compositions, or vaccines, against cancers, infectious or autoimmune  
CC diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or  
CC allergies. They can also be used as immunoassay reagents for diagnosing  
CC these conditions. mig can be used in human or veterinary medicine. mig  
CC have higher affinity or specificity than native antibodies. Manipulation  
CC of CDR ensures binding or specificity and avoids the unpredictable  
CC immunization and screening procedures currently used. It is now possible  
CC to generate antibodies against antigens that are inaccessible, by virtue  
CC of immune tolerance or cryptic expression. mig neutralize antigens  
CC directly or they induce an anti-idiotypic immune response. This sequence  
CC represents a fragment of modified immunoglobulin that immunospecifically  
CC binds to a binding pair in which the first member is the human milk fat  
CC globule antigen  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 6  
AAY95234  
ID AAY95234 standard; peptide; 7 AA.  
XX  
AC AAY95234;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Human monoclonal antibody LEN VL CDR2.  
XX  
KW Human; monoclonal antibody; LEN; humanised antibody; CC49; HuCC49; CDR;  
KW complementarity determining region; colon cancer;  
KW tumor associated glycoprotein-72; TAG-72; tumour marker; carcinoma;  
KW diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FH Region  
FT 1.  
FT /note= "specificity determining region"  
XX  
PN WO200026394-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-US025552.  
XX

DR 31-OCT-1998; 98US-0106534P.  
PR 02-NOV-1998; 98US-0106757P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Kashmiri SVS, Padlan EA, Schlom J;  
XX  
DR WPI; 2000-365637/31.  
XX  
PT Chimeric variants of CC49 monoclonal antibodies useful for detecting and  
PT treating cancers associated with the expression of the pancreaticoma tumor  
PT -associated antigen TAG-72.  
XX  
PS Disclosure; Fig 2; 76pp; English.  
XX  
CC The present sequence is that of complementarity determining region 2 (L-  
CC CDR2) of the light chain variable region (VL) of human monoclonal  
CC antibody LEN. The invention is directed toward mouse-human chimeric  
CC variants of CC49 MAbS with minimal murine content, to methods of making  
CC such variants, and to their therapeutic application. Variants are  
CC provided of huCC49, a humanised MAb formed by grafting hypervariable  
CC regions from murine CC49 into VL and VH frameworks of human MAbS LEN and  
CC 21/28' CL, respectively, while retaining murine framework residues  
CC required for integrity of the antigen combining site structure. HuCC49  
CC binds to the human pancreaticoma tumor associated glycoprotein-72 (TAG-  
CC 72), which is found on the surface of certain human tumours. Novel  
CC variants of huCC49 of the invention have fewer than all 6 CDRs of CC49  
CC present. Also provided are specificity determining region (SDR) variants  
CC of huCC49 in which only SDRs of at least 1 CDR from CC49 are present.  
CC Particular variants of HuCC9 have either L-CDR1 and/or L-CDR2 from human  
CC MAb LEN. These variants have the same or 2-fold lower affinity constant  
CC than HuCC49. They are used in claimed methods of treating cancer and for  
CC detecting cancer cells that express TAG-72  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 7  
AAY32227  
ID AAY32227 standard; peptide; 7 AA.  
XX  
AC AAY32227;

DT 15-FEB-2000 (first entry)

DE G-CSF agonist antibody mAb163-93 light chain variable region CDR2.

KW Granulocyte colony stimulating factor receptor; G-CSF; mouse;  
KW monoclonal antibody; agonist; screening; neutropenia; therapy;  
KW complementarity determining region; CDR; mAb163-93.

OS Mus musculus.

PN WO9955735-A1.

PD 04-NOV-1999.

PF 30-APR-1999; 99WO-US009466.

PR 30-APR-1998; 98US-0083575P.

PA (TANO-) TANOX INC.

PI Nt B, Sun BNC, Sun CRY;

DR WPI; 2000-052805/04.  
XX  
PT Treatment of neutropenia by stimulating proliferation of neutrophilic  
PT cell lineage progenitors.  
XX  
PS Claim 13; Page 30; 64pp; English.  
XX  
CC The present sequence represents complementarity determining region 2  
CC (CDR2) of the light chain variable region of murine monoclonal antibody  
CC mAb163-93. This antibody is an example of an agonist molecule that  
CC specifically binds to or interacts with human granulocyte colony  
CC stimulating factor (G-CSF) receptor to stimulate cell proliferation and  
CC differentiation, especially by dimerising the receptor or activating  
CC phosphorylation of kinases associated with the receptor. Agonist  
CC antibodies can be used to stimulate proliferation of G-CSF-dependent  
CC cells, e.g. to differentiate leading to a repopulation of neutrophilic  
CC granulocyte lineage cells, especially to treat neutropenia (claimed).  
CC They can also be used to detect human G-CSF receptor immunologically  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 8  
AAB07952  
ID AAB07952 standard; peptide; 7 AA.  
XX  
AC AAB07952;

DT 14-NOV-2000 (first entry)

DE CDR2 sequence from an antibody with affinity for B7 molecules.

KW Complementarity determining region; CDR; antibody; B7 molecule; B7-1;  
KW B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;  
KW inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;  
KW insulinitis; asthma; arthritis; inflammatory bowel disease; cancer;  
KW inflammatory dermatitis; multiple sclerosis; transplant rejection;  
KW proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;  
KW thalassemia; aplastic anaemia; myeloid dysplasia syndrome.

OS Mus sp.

PN WO200047625-A2.

PD 17-AUG-2000.

PF 09-FEB-2000; 2000WO-US003303.

PR 12-FEB-1999; 99US-00249011.

PR 24-JUN-1999; 99US-00339596.

PA (GEMV ) GENETICS INST INC.

PI Co MS, Vasquez M, Carrero B, Celniker AC, Collins M, Goldman S;

PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;

DR WPI; 2000-524532/47.

PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRJ-12524) molecules,  
PT modulates immune responses and can therefore treat e.g. autoimmune  
PT diseases, infectious diseases.

PS Disclosure; Page 28; 162pp; English.

CC The present sequence represents a complementarily determining region  
CC (CDR) 2 from the light chains of an murine antibody with having a binding  
CC specificity to B7-2 molecules. The sequence is used to construct  
CC humanized immunoglobulins, which comprise an antigen binding region of  
CC non-human origin and a portion of a human immunoglobulin. The humanized  
CC immunoglobulins are useful for treating autoimmune diseases, infectious  
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
CC also useful for treating a transplant recipient or preventing transplant  
CC rejection in a transplant recipient, and treating proliferative disease  
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome  
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 9  
AAU81257  
ID AAU81257 standard; peptide; 7 AA.  
XX  
AC AAU81257;  
XX  
DT 09-APR-2002 (first entry)  
XX

DE Human trkC antibody light chain CDR2 of variable region #2.  
XX  
XX Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;  
KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;  
KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;  
KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;  
KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;  
KW basopaenia; lymphopaenia; monocytopenia; neutropaenia; cancer; ulcer;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;  
KW cellular degeneration; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200198361-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US020153.  
XX  
PR 22-JUN-2000; 2000US-0213141P.  
PR 05-OCT-2000; 2000US-0238319P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Devaux B, Hongo JS, Presta LG, Shelton DL;  
XX  
XX WPI; 2002-130790/17.  
XX  
DR  
XX  
PT Novel anti-trkC agonist monoclonal antibody useful for treating  
PT neurodegenerative disease, shows no significant cross-reactivity with  
PT trkA/trkB, and recognizes epitope in domain 5 of trkC.  
XX  
PS Claim 13; Fig 11; 121pp; English.  
XX  
XX The invention relates to an anti-trkC agonist monoclonal antibody which  
CC shows no significant cross-reactivity with trkA or trkB, and recognizes  
CC an epitope in domain 5 of trkC. The antibodies of the invention are  
CC effective in the treatment of cisplatin- or pyridoxine-induced

CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre  
CC sensory neuropathy, neurodegenerative disease including amyotrophic  
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood  
CC cells such as leukopaenia including eosinopaenia, basopaenia,  
CC lymphopaenia, monocytopenia, neutropaenia, Alzheimer's disease,  
CC Parkinson's disease, Huntington's disease and tumours. The sequences are  
CC also useful for inducing angiogenesis for treating wounds, ulcers and  
CC diabetic complications of sickle cell disease, for treating cardiac  
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases  
CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent  
CC human and mouse anti-trkC agonist monoclonal antibodies and antibody  
CC fragments of the invention  
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 10  
ABP62361  
ID ABP62361 standard; peptide; 7 AA.  
XX  
AC ABP62361;  
XX  
DT 10-OCT-2002 (first entry)  
XX

DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #38.  
XX  
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KW NS3 protein; viral infection.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200259340-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 25-JAN-2002; 2002WO-US002303.  
XX  
PR 26-JAN-2001; 2001US-0264451P.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
PI Maruyama T, Jones IM, Burton DR, Fox RI;  
XX  
XX WPI; 2002-599801/64.  
XX  
DR  
XX  
PT New human immunopolypeptide with binding specificity for certain envelope  
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for  
PT diagnosing or treating patients having or suspected of having HCV  
PT infection.  
XX  
XX Claim 1; Fig 17; 308pp; English.  
XX  
XX The present invention relates to human immunopolypeptides, produced by a  
CC phage transfected cell library. The present sequence is one such  
CC immunopolypeptide. The immunopolypeptides have binding specificity for  
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
CC cell binding and contains neutralising epitopes, while NS3 is thought to  
CC be involved in the replication of HCV. The immunopolypeptides are useful  
CC for diagnosing and treating a patient having or suspected to be having  
CC HCV infection  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 11  
AAE29275  
ID AAE29275 standard; peptide; 7 AA.  
XX  
AC AAE29275;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Anti-ClfA monoclonal antibody variable light chain CDR2.  
XX  
KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;  
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;  
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;  
KW complementarity determining region; CDR.  
XX  
OS Unidentified.  
XX  
PN WO200272600-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 28-JAN-2002; 2002WO-US002296.  
XX  
PR 26-JAN-2001; 2001US-0264072P.  
PR 12-MAR-2001; 2001US-0274611P.  
PR 18-JUN-2001; 2001US-0298413P.  
PR 30-JUL-2001; 2001US-0308116P.  
XX  
PA (INH1-) INHIBITEX INC.  
XX  
PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;  
XX  
DR WPI; 2002-759834/82.  
XX  
PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for  
PT treating or preventing Staphylococcus aureus infection e.g. wound  
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in  
PT a human or animal.  
XX  
PS Claim 30; Page 55; 80pp; English.  
XX  
CC The invention relates to monoclonal antibody which binds the clumping  
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA  
CC monoclonal antibody is useful for treating or preventing S. aureus  
CC infection in a human or animal, and for inhibiting the binding of  
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment  
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3  
CC protein is useful for inducing an immunological response in a human or  
CC animal. These staphylococcal infections include wound infections, sepsis,  
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The  
CC present sequence is an anti-ClfA monoclonal antibody variable light chain  
CC complementarity determining region (CDR)  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 12  
ABG68854  
ID ABG68854 standard; peptide; 7 AA.  
XX  
AC ABG68854;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE CDR2 VL peptide.  
XX  
KW Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;  
KW immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN;  
KW cancer; haematological malignancy; viral infection; hepatitis; human;  
KW multiple sclerosis; autoimmune disease; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200244197-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 30-NOV-2001; 2001WO-CA001701.  
XX  
PR 01-DEC-2000; 2000US-00727388.  
XX  
PA (FISH/) FISH E N.  
XX  
PI Fish EN;  
XX  
DR WPI; 2002-547689/58.  
DR N-PSDB; ABK97817.  
XX

Cytokine receptor binding peptide construct, in particular interferon  
PT receptor binding peptide construct for use as an interferon mimetic,  
PT comprises a cytokine receptor binding domain incorporated in a molecular  
PT scaffold.  
XX  
XX  
PS Example 8; Page 50; 105pp; English.

CC This invention relates to a novel cytokine receptor binding peptide  
CC construct comprising a cytokine receptor binding domain incorporated in a  
CC suitable molecular scaffold so that the scaffold maintains the binding  
CC domain in a configuration suitable for binding to the cytokine receptor.  
CC The peptides of the invention may have cytostatic, virucide,  
CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and  
CC antiarthritic activities. A new interferon receptor binding peptide  
CC construct is useful in the manufacture of a medicament as an interferon  
CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in  
CC medical therapies for cancer, haematological malignancies, viral  
CC infections (hepatitis B or C), multiple sclerosis and autoimmune diseases  
CC such as arthritis, to detect modulators of IFN action, in screening  
CC assays to compare the activity and/or interaction with another molecule  
CC or potential IFN modulator and also in the diagnosis of IFN activity  
CC related disorders. A nucleic acid encoding the peptide of the invention  
CC or is useful for the treatment and therapy of the mentioned medical  
CC conditions. The peptide of the invention has less side effect than those  
CC of native cytokines. The present sequence represents an interferon  
CC receptor binding peptide of the invention  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 13  
AAU70347  
ID AAU70347 standard; peptide; 7 AA.



XX AAV70347;  
AC  
XX 14-FEB-2002 (first entry)  
DT  
XX  
DE Mouse Kappa I light chain CDR2.  
XX  
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IGBP;  
KW transgenic plant; immunoglobulin binding protein array; IGM; IGG; IGA;  
KM IGD; IGE; IGY; IGM; kappa; lambda; CHBP.  
XX  
OS Mus musculus.  
XX  
PN WO200183806-A1.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014349.  
XX  
PR 02-MAY-2000; 2000US-00563222.  
XX  
PA (EPIC-) EPICYTE PHARM INC.  
XX  
PI Hiatt AC, Hein MB;  
PI  
XX  
DR WPI; 2002-055482/07.  
XX  
PT Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
XX  
PS Disclosure; Page 14; 129pp; English.  
XX  
CC The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IGBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IGBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IGBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IGM, IGG, IGA,  
CC IGD, IGE, IGY, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably  
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IGBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IGBP of the invention  
XX  
XX Sequence 7 AA;  
SO  
Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 14  
AAU70335  
ID AAV70335 standard; peptide; 7 AA.  
XX  
AC AAV70335;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human Kappa IV light chain CDR2.  
XX

KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IGBP;  
KW transgenic plant; immunoglobulin binding protein array; IGM; IGG; IGA;  
KM IGD; IGE; IGY; IGM; kappa; lambda; CHBP.  
XX  
OS Homo sapiens.  
XX  
PN WO200183806-A1.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014349.  
XX  
PR 02-MAY-2000; 2000US-00563222.  
XX  
PA (EPIC-) EPICYTE PHARM INC.  
XX  
PI Hiatt AC, Hein MB;  
PI  
XX  
DR WPI; 2002-055482/07.  
XX  
PT Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
XX  
PS Disclosure; Page 14; 129pp; English.  
XX  
CC The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IGBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IGBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IGBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IGM, IGG, IGA,  
CC IGD, IGE, IGY, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably  
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IGBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IGBP of the invention  
XX  
XX Sequence 7 AA;  
SO  
Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 15  
AAE34369  
ID AAE34369 standard; peptide; 7 AA.  
XX  
AC AAE34369;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
DE Escherichia coli light chain variable region CDR2.  
XX  
KW S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;  
KW hepatotropic; complementarity determining region; CDR.  
OS Escherichia coli.  
XX  
PN WO200292819-A1.  
XX



PD	21-NOV-2002.	
XX		
PF	15-MAY-2002; 2002WO-KR000905.	
XX		
PR	16-MAY-2001; 2001KR-00026634.	
XX		
PA	(YUHA-) YUHAN CORP.	
XX		
PI	Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;	
XX		
DR	WPI; 2003-140281/13.	
XX		
PT	New light and heavy chain variable regions of a monoclonal antibody	
PT	against the S-surface antigen of the hepatitis B virus (HBV), useful for	
PT	neutralizing or removing HBV, or for preventing or treating HBV	
PT	infection.	
XX		
PS	Claim 11; Page 17; 20pp; English.	
XX		
CC	The invention relates to light and heavy chain variable regions of a	
CC	monoclonal antibody against S-surface antigen of the hepatitis B virus	
CC	(HBV). The variable regions of the antibodies are useful against HBV S-	
CC	surface antigens, e.g. adr, adw, ayr or ayw, particularly for	
CC	neutralising or removing HBV. They may also be employed to treat or	
CC	prevent HBV infection. The present sequence is Escherichia coli light	
CC	chain variable region complementarity determining region (CDR)	
XX		
SQ	Sequence 7 AA;	
	Query Match	100.0%; Score 38; DB 6; Length 7;
	Best Local Similarity	100.0%; Pred. No. 1.8e+06;
	Matches 7; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 WASTRES 7.	
Db	1 WASTRES 7	

Search completed: March 1, 2005, 17:36:08  
Job time : 53.3385 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 13.6769 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	1 US-08-360-125-20	Sequence 20, Appl
2	38	100.0	7	2 US-08-450-578-20	Sequence 20, Appl
3	38	100.0	7	2 US-09-017-628-20	Sequence 20, Appl
4	38	100.0	7	2 US-09-014-880-20	Sequence 20, Appl
5	38	100.0	7	3 US-07-987-264-5	Sequence 5, Appl
6	38	100.0	7	4 US-08-450-363-20	Sequence 20, Appl
7	38	100.0	7	4 US-09-563-222C-15	Sequence 15, Appl
8	38	100.0	7	4 US-09-467-903-20	Sequence 27, Appl
9	38	100.0	7	4 US-09-563-222C-27	Sequence 20, Appl
10	38	100.0	7	4 US-09-830-748B-8	Sequence 8, Appl
11	38	100.0	7	4 US-09-627-896B-18	Sequence 18, Appl
12	38	100.0	7	5 PCT-US93-08435-24	Sequence 24, Appl
13	38	100.0	7	5 PCT-US93-08435-37	Sequence 37, Appl
14	38	100.0	7	5 PCT-US93-08435-41	Sequence 41, Appl
15	38	100.0	101	4 US-09-627-896B-28	Sequence 28, Appl
16	38	100.0	109	2 US-08-308-494A-23	Sequence 23, Appl
17	38	100.0	110	3 US-08-957-001B-5	Sequence 5, Appl
18	38	100.0	110	3 US-08-957-001B-24	Sequence 24, Appl
19	38	100.0	110	3 US-09-496-301-5	Sequence 5, Appl
20	38	100.0	110	3 US-09-496-301-24	Sequence 24, Appl
21	38	100.0	112	1 US-07-942-245-30	Sequence 30, Appl
22	38	100.0	112	2 US-07-916-098A-15	Sequence 15, Appl
23	38	100.0	112	4 US-08-435-516-4	Sequence 4, Appl
24	38	100.0	112	4 US-08-435-516-28	Sequence 28, Appl
25	38	100.0	113	1 US-08-690-102A-2	Sequence 2, Appl
26	38	100.0	113	1 US-08-690-102A-6	Sequence 6, Appl
27	38	100.0	113	3 US-08-483-749A-16	Sequence 16, Appl

28	38	100.0	113	3 US-09-127-902-2	Sequence 2, Appl
29	38	100.0	113	3 US-09-127-902-6	Sequence 6, Appl
30	38	100.0	113	3 US-09-155-107-2	Sequence 2, Appl
31	38	100.0	113	3 US-09-155-107-6	Sequence 6, Appl
32	38	100.0	113	3 US-09-155-107-20	Sequence 20, Appl
33	38	100.0	113	3 US-08-525-539A-80	Sequence 80, Appl
34	38	100.0	113	4 US-09-301-593-2	Sequence 2, Appl
35	38	100.0	113	4 US-09-301-593-4	Sequence 4, Appl
36	38	100.0	113	4 US-09-301-593-6	Sequence 6, Appl
37	38	100.0	113	4 US-09-301-593-32	Sequence 32, Appl
38	38	100.0	113	4 US-09-301-593-33	Sequence 33, Appl
39	38	100.0	113	4 US-09-301-593-34	Sequence 34, Appl
40	38	100.0	113	5 US-09-274-163E-16	Sequence 16, Appl
41	38	100.0	113	5 PCT-US93-08435-4	Sequence 4, Appl
42	38	100.0	113	5 PCT-US93-08435-6	Sequence 6, Appl
43	38	100.0	113	5 PCT-US93-08435-8	Sequence 8, Appl
44	38	100.0	113	5 PCT-US93-11611-5	Sequence 5, Appl
45	38	100.0	113	5 PCT-US95-09641-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-360-125-20  
; Sequence 20, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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: HYPOTHETICAL:
: ANTI-SENSE:
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM:
: STRAIN:
: INDIVIDUAL ISOLATE:
: DEVELOPMENTAL STAGE:
: HAPLOTYPE:
: TISSUE TYPE:
: CELL TYPE: Hybridoma producing human antibody GAH
: CELL LINE:
: ORGANELLE:
: IMMEDIATE SOURCE:
: LIBRARY:
: CLONE:
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT:
: MAP POSITION:
: UNITS:
: FEATURE:
: NAME/KEY:
: LOCATION:
: IDENTIFICATION METHOD:
: OTHER INFORMATION:
: PUBLICATION INFORMATION:
: AUTHORS:
: TITLE:
: JOURNAL:
: VOLUME:
: ISSUE:
: PAGES:
: DATE:
: DOCUMENT NUMBER:
: FILING DATE:
: PUBLICATION DATE:
: RELEVANT RESIDUES IN SEQ ID NO:
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: US-08-360-125-20
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: Query Match      100.0%; Score 38; DB 1; Length 7;
: Best Local Similarity 100.0%; Pred. No. 4.1e+05;
: Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY      1 WASTRES 7
:         |||||
:         1 WASTRES 7
:
: Db
:
: RESULT 2
: US-08-450-578-20
: Sequence 20, Application US/08450578
: Patent No. 5837845
: GENERAL INFORMATION:
: APPLICANT: Saiko HOSOKAWA
: APPLICANT: Toshiki TAGAWA
: APPLICANT: Yoko HIRAKAWA
: APPLICANT: No. 5837845hiko ITO
: APPLICANT: Kazuhito NAGAIKE
: TITLE OF INVENTION: Human Monoclonal Antibody
: TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
: TITLE OF INVENTION: Cell Membrane
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wenderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS

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: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/450,578
: FILING DATE: May 25, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/360,125
: FILING DATE: December 20, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/905,534
: FILING DATE: June 29, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Warren M. Cheek, Jr.
: REGISTRATION NUMBER: 33,367
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-8850
: TELEFAX:
: TELEX:
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL:
: ANTI-SENSE:
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM:
: STRAIN:
: INDIVIDUAL ISOLATE:
: DEVELOPMENTAL STAGE:
: HAPLOTYPE:
: TISSUE TYPE:
: CELL TYPE: Hybridoma producing human antibody GAH
: CELL LINE:
: ORGANELLE:
: IMMEDIATE SOURCE:
: LIBRARY:
: CLONE:
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT:
: MAP POSITION:
: UNITS:
: FEATURE:
: NAME/KEY:
: LOCATION:
: IDENTIFICATION METHOD:
: OTHER INFORMATION:
: PUBLICATION INFORMATION:
: AUTHORS:
: TITLE:
: JOURNAL:
: VOLUME:
: ISSUE:
: PAGES:
: DATE:
: DOCUMENT NUMBER:
: FILING DATE:
: PUBLICATION DATE:
: RELEVANT RESIDUES IN SEQ ID NO:
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: US-08-450-578-20
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: Query Match      100.0%; Score 38; DB 2; Length 7;
: Best Local Similarity 100.0%; Pred. No. 4.1e+05;
: Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY      1 WASTRES 7
:         |||||
:         1 WASTRES 7
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: Db

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RESULT 3  
US-09-017-628-20  
; Sequence 20, Application US/09017628  
; Patent No. 5990287  
; GENERAL INFORMATION:  
; APPLICANT: HOSOKAWA, Saiko  
; APPLICANT: TAGAWA, Toshiaki  
; APPLICANT: HIRAKAWA, Yoko  
; APPLICANT: ITO, No. 5990287ihiko  
; APPLICANT: NAGAIKE, Kazuhiro  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; FILE REFERENCE: 177/527361KH  
; CURRENT APPLICATION NUMBER: US/09/017,628  
; CURRENT FILING DATE: 1998-02-02  
; EARLIER APPLICATION NUMBER: 08/360,125  
; EARLIER FILING DATE: 1994-12-20  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-20

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
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Db 1 WASTRES 7

RESULT 4  
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; Sequence 20, Application US/09014880  
; Patent No. 5990297  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA et al.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
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; APPLICATION NUMBER: US/09/014,880  
; FILING DATE: January 28, 1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/450,578  
; FILING DATE: May 25, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; CELL TYPE: Hybridoma producing human antibody GAH  
US-09-014-880-20

OY 1 WASTRES 7  
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Db 1 WASTRES 7

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
US-07-987-264-5  
; Sequence 5, Application US/07987264  
; Patent No. 6204366  
; GENERAL INFORMATION:  
; APPLICANT: VERHOEVEN, MARTINE ELISA  
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/987,264  
; FILING DATE: 08-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9019553.8  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB PCT/GB91/01511  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 200232/P3095USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-987-264-5

Query Match 100.0%; Score 38; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7  
Db 1 WASTRES 7

RESULT 6  
US-08-450-363-20  
; Sequence 20, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 142  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,363  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE: Hybridoma producing human antibody GAH  
; CELL LINE:  
; ORGANELLE:

; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-363-20

Query Match 100.0%; Score 38; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7  
Db 1 WASTRES 7

RESULT 7  
US-09-563-222C-15  
; Sequence 15, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-563-222C-15

Query Match 100.0%; Score 38; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7  
Db 1 WASTRES 7

RESULT 8  
US-09-563-222C-27  
; Sequence 27, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:



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; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-27

Query Match      100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 WASTRES 7
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        1 WASTRES 7

Db      1 WASTRES 7

RESULT 9
US-09-467-903-20
; Sequence 20, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
;          Yoshiaki TAGAWA
;          Yoko HIRAKAWA
;          No. 6787153;hiko ITO
;          Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
;                   Specifically Binding to Surface Antigen of Cancer
;                   Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,903
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,363
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER: JP158859/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158860/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158861/1991
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
```

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; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; STRAIN: <Unknown>
; INDIVIDUAL ISOLATE: <Unknown>
; DEVELOPMENTAL STAGE: <Unknown>
; HAPLOTYPE: <Unknown>
; TISSUE TYPE: <Unknown>
; CELL TYPE: Hybridoma producing human antibody GAH
; CELL LINE: <Unknown>
; ORGANELLE: <Unknown>
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: <Unknown>
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: <Unknown>
; MAP POSITION: <Unknown>
; UNITS: <Unknown>
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-467-903-20

Query Match      100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 WASTRES 7
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        1 WASTRES 7

Db      1 WASTRES 7

RESULT 10
US-09-830-748B-8
; Sequence 8, Application US/09830748B
; Patent No. 6818749
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by The
;           Secretary of the Department of Health and Human Services
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jeffery, Schlom
; TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
; FILE REFERENCE: 4239-61725
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; CURRENT APPLICATION NUMBER: US/09/830,748B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: PCT/ US99/25552
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,757
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 60/106,534
; PRIOR FILING DATE: 1998-10-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-830-748B-8
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Query Match      100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 WASTRES 7
        |||||||
Db      1 WASTRES 7
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## RESULT 11

```
US-09-627-896B-18
; Sequence 18, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized
; OTHER INFORMATION: murine anti-human B7-2 light chain
; US-09-627-896B-18
```

```
Query Match      100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 WASTRES 7
        |||||||
Db      1 WASTRES 7
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## RESULT 12

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PCT-US93-08435-24
; Sequence 24, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
```

```
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US93-08435-24
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Query Match      100.0%; Score 38; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 WASTRES 7
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Db      1 WASTRES 7
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## RESULT 13

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PCT-US93-08435-37
; Sequence 37, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US93/08435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,654  
FILING DATE: 09-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: SBC P50107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9200  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US93-08435-37

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 14  
PCT-US93-08435-41  
Sequence 41, Application PC/TUS9308435  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham, Corporation  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Navy  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Army  
TITLE OF INVENTION: Novel Antibodies for Confering Passive  
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 Norristown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,654  
FILING DATE: 09-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: SBC P50107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9200  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

MOLECULE TYPE: protein  
PCT-US93-08435-41

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 15  
US-09-627-896B-28  
Sequence 28, Application US/09627896B  
Patent No. 6827934  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARRENO, BEATRIZ  
APPLICANT: CELINKER, ABBIE CHERYL  
APPLICANT: GOLDMAN, MARY  
APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VELDMAN, GEERTRUIDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
TITLE OF INVENTION: OF TREATMENT THEREWITH  
FILE REFERENCE: 08702.0081-01000  
CURRENT APPLICATION NUMBER: US/09/627, 896B  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 28  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: H2F light chain variable region  
US-09-627-896B-28

Query Match 100.0%; Score 38; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 56 WASTRES 62

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Job time : 13.6769 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 37.4769 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	9	US-09-749-831-5 Sequence 5, Appli
2	38	100.0	7	9	US-09-828-708-43 Sequence 43, Appl
3	38	100.0	7	9	US-09-828-708-46 Sequence 46, Appl
4	38	100.0	7	9	US-09-249-011A-18 Sequence 18, Appl
5	38	100.0	7	10	US-09-563-222-15 Sequence 15, Appl
6	38	100.0	7	10	US-09-563-222-27 Sequence 27, Appl
7	38	100.0	7	13	US-10-146-305-10 Sequence 10, Appl
8	38	100.0	7	14	US-10-071-962-19 Sequence 19, Appl
9	38	100.0	7	16	US-10-312-316-29 Sequence 29, Appl
10	38	100.0	7	16	US-10-469-125-5 Sequence 5, Appli
11	38	100.0	7	16	US-10-783-950-15 Sequence 15, Appl
12	38	100.0	7	16	US-10-783-950-27 Sequence 27, Appl
13	38	100.0	7	17	US-10-483-994-5 Sequence 5, Appli

14	38	100.0	7	17	US-10-483-993-5	Sequence 5, Appli
15	38	100.0	82	14	US-10-078-958-15	Sequence 15, Appl
16	38	100.0	94	9	US-09-905-243-60	Sequence 60, Appl
17	38	100.0	101	14	US-10-194-975-89	Sequence 89, Appl
18	38	100.0	101	14	US-10-125-687-25	Sequence 25, Appl
19	38	100.0	101	15	US-10-308-817-36	Sequence 36, Appl
20	38	100.0	101	15	US-10-453-698-36	Sequence 36, Appl
21	38	100.0	101	16	US-10-379-392-103	Sequence 103, App
22	38	100.0	105	14	US-10-010-729-37	Sequence 37, Appl
23	38	100.0	107	14	US-10-325-694-142	Sequence 142, App
24	38	100.0	107	14	US-10-325-694-148	Sequence 148, App
25	38	100.0	107	14	US-10-325-694-149	Sequence 149, App
26	38	100.0	107	14	US-10-325-694-152	Sequence 152, App
27	38	100.0	109	9	US-09-828-708-1	Sequence 1, Appli
28	38	100.0	109	9	US-09-828-708-4	Sequence 4, Appli
29	38	100.0	112	14	US-10-056-052-6	Sequence 6, Appli
30	38	100.0	112	14	US-10-056-052-10	Sequence 10, Appl
31	38	100.0	112	14	US-10-056-052-14	Sequence 14, Appl
32	38	100.0	112	14	US-10-056-052-18	Sequence 18, Appl
33	38	100.0	112	14	US-10-229-335-4	Sequence 4, Appli
34	38	100.0	112	14	US-10-229-335-28	Sequence 28, Appl
35	38	100.0	113	9	US-09-301-593-2	Sequence 2, Appli
36	38	100.0	113	9	US-09-301-593-4	Sequence 4, Appli
37	38	100.0	113	9	US-09-301-593-6	Sequence 6, Appli
38	38	100.0	113	9	US-09-301-593-32	Sequence 32, Appl
39	38	100.0	113	9	US-09-301-593-33	Sequence 33, Appl
40	38	100.0	113	9	US-09-301-593-34	Sequence 34, Appl
41	38	100.0	113	9	US-09-741-843-2	Sequence 2, Appli
42	38	100.0	113	9	US-09-741-843-6	Sequence 6, Appli
43	38	100.0	113	9	US-09-274-163E-16	Sequence 16, Appl
44	38	100.0	113	9	US-09-956-206A-80	Sequence 80, Appl
45	38	100.0	113	10	US-09-894-839-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-749-831-5  
; Sequence 5, Application US/09749831  
; Publication No. US20020086978A1  
; GENERAL INFORMATION:  
; APPLICANT: VERHOEVEN, MARTINE ELISA  
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop LLP  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/749, 831  
; FILING DATE: 04-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/987, 264  
; FILING DATE: 08-MAR-1993  
; APPLICATION NUMBER: GB PCT/GB91/01511  
; FILING DATE: 05-SEP-1991  
; APPLICATION NUMBER: GB 9019553.8  
; FILING DATE: 07-SEP-1990  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single



TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5  
US-09-749-831-5

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 2  
US-09-828-708-43  
Sequence 43, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-43

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 3  
US-09-828-708-46  
Sequence 46, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 46  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-46

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 4  
US-09-249-011A-18  
Sequence 18, Application US/09249011A  
Patent No. US20020176855A1  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARRENO, BEATRIZ  
APPLICANT: CELNIKER, ABBIE CHERYL  
APPLICANT: COLLINS, MARY  
APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VELDMAN, GEERTRUIDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
FILE REFERENCE: 08702.0081-00000  
CURRENT APPLICATION NUMBER: US/09/249,011A  
CURRENT FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized  
US-09-249-011A-18

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 5  
US-09-563-222-15  
Sequence 15, Application US/09563222  
Publication No. US20030079253A1  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Hein, Mich B.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
FILE REFERENCE: 310098.406  
CURRENT APPLICATION NUMBER: US/09/563,222  
CURRENT FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-563-222-15

Query Match 100.0%; Score 38; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
| | | | |  
Db 1 WASTRES 7

RESULT 6  
US-09-563-222-27

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; Sequence 27, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 31098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-27
```

```
Query Match      100.0%; Score 38; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
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RESULT 7
US-10-146-305-10
; Sequence 10, Application US/10146305
; Publication No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE REFERENCE: OVI7440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-10
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Query Match      100.0%; Score 38; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
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RESULT 8
US-10-071-962-19
; Sequence 19, Application US/10071962
; Publication No. US20030170237A1
; GENERAL INFORMATION:
; APPLICANT: BauFu Ni
; APPLICANT: Bill N.C. Sun
; APPLICANT: Cedily R.Y. Sun
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
; FILE REFERENCE: 98-3
; CURRENT APPLICATION NUMBER: US/10/071,962
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/303,155A
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,575
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; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-10-071-962-19
```

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Query Match      100.0%; Score 38; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
```

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RESULT 9
US-10-312-316-29
; Sequence 29, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT 040QPC
; CURRENT APPLICATION NUMBER: US/10/312,316
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/238,319
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-29
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Query Match      100.0%; Score 38; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WASTRES 7
        |||||
Db      1 WASTRES 7
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RESULT 10
US-10-469-125-5
; Sequence 5, Application US/10469125
; Publication No. US20040143101A1
; GENERAL INFORMATION:
; APPLICANT: Soltis, Daniel A.
; APPLICANT: Burch, Ronald M.
; APPLICANT: Shukla, Rajiv
; TITLE OF INVENTION: IMMUNOGLOBULIN CONSTRUCT CONTAINING ANTI-MUCIN VARIABLE DOMAIN SE
; FILE REFERENCE: 02755/100G273-US1
; CURRENT APPLICATION NUMBER: US/10/469,125
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: US 60/281,182
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/US02/10304
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Homo sapiens  
US-10-469-125-5

Query Match 100.0%; Score 38; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 11  
US-10-783-950-15

; Sequence 15, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-783-950-15

Query Match 100.0%; Score 38; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 12  
US-10-783-950-27

; Sequence 27, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-783-950-27

Query Match 100.0%; Score 38; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 13  
US-10-483-994-5

; Sequence 5, Application US/10483994  
; Publication No. US20050032132A1  
; GENERAL INFORMATION:  
; APPLICANT: MITSUBISHI PHARMA CORPORATION  
; TITLE OF INVENTION: CANCER DIAGNOSTICS  
; FILE REFERENCE: 02031WO0  
; CURRENT APPLICATION NUMBER: US/10/483,994  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: JP P2001-224054  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-483-994-5

Query Match 100.0%; Score 38; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 14  
US-10-483-993-5

; Sequence 5, Application US/10483993  
; Publication No. US20050037061A1  
; GENERAL INFORMATION:  
; APPLICANT: MITSUBISHI PHARMA CORPORATION  
; TITLE OF INVENTION: REMDIES FOR MAMMARY CANCER  
; FILE REFERENCE: 02031WO0  
; CURRENT APPLICATION NUMBER: US/10/483,993  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: JP P2001-224596  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-483-993-5

Query Match 100.0%; Score 38; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||  
Db 1 WASTRES 7

RESULT 15  
US-10-078-958-15

; Sequence 15, Application US/10078958  
; Publication No. US20030070185A1  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBYITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN

; APPLICANT: MENDEZ, MICHAEL J.  
; APPLICANT: GREEN, LARRY  
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING  
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED  
; TITLE OF INVENTION: THEREFROM  
; FILE REFERENCE: CELL 4.18 CON  
; CURRENT APPLICATION NUMBER: US/10/078,958  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 08/759,620  
; PRIOR FILING DATE: 1996-12-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-078-958-15

Query Match 100.0%; Score 38; DB 14; Length 82;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WASTRES 7  
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Db 37 WASTRES 43

Search completed: March 1, 2005, 17:52:51  
Job time : 37.4769 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 9.47692 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	100.0	81	2	PH1048	Ig light chain V r
2	38	100.0	92	2	S37532	Ig kappa chain V r
3	38	100.0	92	2	S37533	Ig kappa chain V r
4	38	100.0	92	2	S37530	Ig kappa chain V r
5	38	100.0	92	2	S37535	Ig kappa chain V r
6	38	100.0	92	2	S37531	Ig kappa chain V r
7	38	100.0	92	2	S37534	Ig kappa chain V r
8	38	100.0	92	2	S37529	Ig kappa chain V r
9	38	100.0	98	2	S19974	Ig kappa chain V r
10	38	100.0	101	2	PH0869	Ig kappa chain V r
11	38	100.0	101	2	PH1046	Ig light chain V r
12	38	100.0	101	2	S26337	Ig light chain V r
13	38	100.0	102	2	A34153	Ig kappa chain V-I
14	38	100.0	103	2	PH1047	Ig light chain V r
15	38	100.0	103	2	PH1051	Ig light chain V r
16	38	100.0	103	2	PH1052	Ig light chain V r
17	38	100.0	103	2	PH1050	Ig light chain V r
18	38	100.0	103	2	PH1054	Ig light chain V r
19	38	100.0	104	2	PH1101	Ig light chain V r
20	38	100.0	104	2	F38601	Ig kappa chain V r
21	38	100.0	104	2	PH1102	Ig light chain V r
22	38	100.0	104	2	PH1103	Ig light chain V r
23	38	100.0	104	2	PH1104	Ig light chain V r
24	38	100.0	106	2	A49138	Ig kappa rheumato
25	38	100.0	111	2	S03304	Ig kappa chain V r
26	38	100.0	111	2	G30502	Ig kappa chain V r
27	38	100.0	112	2	S09970	Ig kappa chain V-J
28	38	100.0	112	2	PL0265	Ig kappa chain V r
29	38	100.0	112	2	S43103	Ig kappa chain V-J

30	38	100.0	113	2	S34002	Ig kappa chain V r
31	38	100.0	113	2	S34003	Ig kappa chain V r
32	38	100.0	113	2	S30523	Ig kappa chain V r
33	38	100.0	113	2	PL0263	Ig kappa chain V r
34	38	100.0	114	2	K4HULN	Ig kappa chain V-I
35	38	100.0	114	2	S44119	Ig kappa chain V-J
36	38	100.0	114	2	S44116	Ig kappa chain V-J
37	38	100.0	118	2	PT0356	Ig kappa chain V r
38	38	100.0	120	2	S51147	antibody light cha
39	38	100.0	120	2	G33932	Ig kappa chain pre
40	38	100.0	121	1	K4HU	Ig kappa chain pre
41	38	100.0	129	2	S40329	Ig kappa chain V-J
42	38	100.0	129	2	S40347	Ig kappa chain V-J
43	38	100.0	133	1	K4HUI	Ig kappa chain - h
44	38	100.0	133	2	PS0023	Ig kappa chain pre
45	38	100.0	134	2	S49531	anti-Sm antibody V

ALIGNMENTS

RESULT 1  
PH1048  
Ig light chain V region (clone 165.49) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996  
C;Accession: PH1048  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Maxton, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1048  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-81 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin

Query Match  
Best Local Similarity 100.0%; Score 38; DB 2; Length 81;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WASTRES 7  
Db 35 WASTRES 41

RESULT 2  
S37532  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37532  
R;Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A;Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood  
A;Reference number: S37501  
A;Accession: S37532  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLB>  
A;Cross-references: EMBL:Z26628; NID:9405706; PIDN:CAA81381.1; PID:9405707  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WASTRES 7  
Db 34 WASTRES 40

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RESULT 3
S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37533
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26627; NID:g405708; PIDN:CAA81380.1; PID:g405709
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 34 WASTRES 40
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RESULT 4
S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37530
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26630; NID:g405702; PIDN:CAA81383.1; PID:g405703
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 34 WASTRES 40

RESULT 5
S37535
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26625; NID:g405712; PIDN:CAA81378.1; PID:g405713
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

```
Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 34 WASTRES 40
```

```
RESULT 6
S37531
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37531
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood,
A:Reference number: S37501
A:Accession: S37531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26629; NID:g405704; PIDN:CAA81382.1; PID:g405705
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

```
Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 34 WASTRES 40
```

```
RESULT 7
S37534
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood,
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26626; NID:g405710; PIDN:CAA81379.1; PID:g405711
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

```
Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 34 WASTRES 40
```

```
RESULT 8
S37529
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood,
```

A;Reference number: S37501  
A;Accession: S37529  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26631; NID:g405700; PIDN:CAA81384.1; PID:g405701  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 34 WASTRES 40

RESULT 9  
Ig kappa chain V region (M-T406) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S19974  
R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19974  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-98 <WEI>  
A;Cross-references: EMBL:X65096; NID:g52294; PIDN:CAA46224.1; PID:g52295  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-80/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 40 WASTRES 46

RESULT 10  
PH0869  
Ig kappa chain V region (anti-DNA, H2F) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
C;Accession: PH0869  
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991  
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype  
A;Reference number: PH0862; MUID:92078875; PMID:1660528  
A;Accession: PH0869  
A;Molecule type: DNA  
A;Residues: 1-101 <MAN>  
A;Note: residues 28-33 were obtained from Figure 4  
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-23/Region: framework 1  
F;16-96/Domain: immunoglobulin homology <IMM>  
F;24-40/Region: complementarity-determining 1  
F;41-55/Region: framework 2  
F;56-62/Region: complementarity-determining 2  
F;63-94/Region: framework 3  
F;95-101/Region: complementarity-determining 3

Query Match 100.0%; Score 38; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WASTRES 7  
|||||  
Db 56 WASTRES 62

RESULT 11  
PH1046  
Ig light chain V region (clone 202.9) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1046  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1046  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-101 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 56 WASTRES 62

RESULT 12  
S26337  
Ig light chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 20-Jun-2000  
C;Accession: S26337; S78449  
R;Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A;Reference number: S26309; MUID:91341421; PMID:1908510  
A;Accession: S26337  
A;Molecule type: mRNA  
A;Residues: 1-101 <STA>  
A;Cross-references: EMBL:X59193  
R;Caton, A.J.  
submitted to the EMBL Data Library, April 1991  
A;Reference number: S78447  
A;Accession: S78449  
A;Molecule type: mRNA  
A;Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>  
A;Cross-references: EMBL:X59193; NID:g52323; PIDN:CAA41903.1; PID:g1334067  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 48 WASTRES 54

RESULT 13  
A34153  
Ig kappa chain V-IV region (Dep) - human  
C;Species: Homo sapiens (man)

C;Date: 11-Apr-1990 #sequence\_revision 11-Apr-1990 #text\_change 21-Jan-2000  
C;Accession: A34153  
R;Mihaesco, E.; Ayadi, H.; Congy, N.; Gendon, M.C.; Roy, J.P.; Heyermann, H.; Frangione  
J. Biol. Chem. 264, 21481-21485, 1989  
A;Title: Multiple mutations in the variable region of the kappa light chains of three mc  
A;Reference number: A34153; MUID:90094313; PMID:2480953  
A;Accession: A34153  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-102 <MIH>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WASTRES 7  
|||  
Db 56 WASTRES 62

RESULT 14  
PH1047  
Ig light chain V region (clones 165.45 and 163-cl) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1047; PH1049  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1047  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-103 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WASTRES 7  
|||  
Db 56 WASTRES 62

RESULT 15  
PH1051  
Ig light chain V region (clone 165.3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1051  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1051  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-103 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 56 WASTRES 62

Search completed: March 1, 2005, 17:44:46  
Job time : 9.47692 secs



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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 45.3385 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	38	100.0	109	1 KV4D_HUMAN	P83593 homo sapien
2	38	100.0	114	1 KV4A_HUMAN	P01625 homo sapien
3	38	100.0	121	1 KV40_HUMAN	P06312 homo sapien
4	38	100.0	133	1 KV4B_HUMAN	P06313 homo sapien
5	38	100.0	134	1 KV4C_HUMAN	P06314 homo sapien
6	35	92.1	130	2 Q9NP29	Q9np29 homo sapien
7	34	89.5	934	2 Q6G2K3	Q6g2k3 bartonella
8	34	89.5	980	2 Q8PL66	Q8pl66 xanthomonas
9	33	86.8	266	2 Q6PJU5	Q6pjus homo sapien
10	33	86.8	1317	2 Q8TFZ3	Q8tfz3 aspergillus
11	32	84.2	347	2 Q915J7	Q915j7 pseudomonas
12	32	84.2	458	2 Q7XUI8	Q7xui8 oryza sativ
13	32	84.2	685	1 SYM_NEIMA	Q9jwp0 neisseria m
14	31	81.6	71	2 Q7QYCI	Q7qyci giardia lam
15	31	81.6	171	2 Q9NSV2	Q9nsv2 caenorhabdi
16	31	81.6	177	2 Q6Z1F0	Q6z1f0 oryza sativ
17	31	81.6	183	2 Q57000	Q57000 zymomonas m
18	31	81.6	226	2 Q88087	Q88087 enterococcu
19	31	81.6	230	2 Q8NU75	Q8nu75 corynebacte
20	31	81.6	338	2 Q7ZQV2	Q7zqv2 human immun
21	31	81.6	338	2 Q7ZQV3	Q7zqv3 human immun
22	31	81.6	340	2 Q7ZQV5	Q7zqv5 human immun
23	31	81.6	382	1 THRC_SYNY3	P74193 synechocyst
24	31	81.6	404	1 YQ19_TREDE	Q73jff treponema d
25	31	81.6	404	2 Q9AMJ2	Q9amj2 streptomyce
26	31	81.6	466	2 Q6AVV5	Q6avv5 oryza sativ
27	31	81.6	504	2 Q64QF9	Q64qf9 bacteroides
28	31	81.6	564	2 Q9NA93	Q9na93 caenorhabdi
29	31	81.6	572	2 Q92X10	Q92x10 rhizobium m
30	31	81.6	642	2 Q8RMG0	Q8rmg0 nostoc sp.
31	31	81.6	642	2 Q8Z0C9	Q8z0c9 anabaena sp

32	31	81.6	642	2 Q9A8Q5	Q9a8q5 caulobacter
33	31	81.6	727	2 Q9BNW8	Q9bnw8 scutigerelel
34	31	81.6	735	2 Q989J7	Q989j7 rhizobium 1
35	31	81.6	783	2 Q8KJN0	Q8kjin0 rhizobium 1
36	31	81.6	875	2 Q7RWP2	Q7rwp2 neurospora
37	31	81.6	1336	2 Q6MP53	Q6mp53 bdellovibri
38	31	81.6	1489	2 Q9LH44	Q9lh44 arabidopsis
39	30	78.9	29	2 Q8C837	Q8c837 mus musculu
40	30	78.9	62	2 Q8B8F5	Q8b8f5 hepatitis b
41	30	78.9	78	2 Q80W72	Q80w72 mus musculu
42	30	78.9	94	2 Q7SEH6	Q7seh6 neurospora
43	30	78.9	103	2 Q8Z272	Q8z272 pyrobaculum
44	30	78.9	118	2 Q9BGP0	Q9bgp0 macaca fasc
45	30	78.9	119	2 Q8JYY1	Q8jyy1 hepatitis b

## ALIGNMENTS

RESULT 1					
ID	KV4D_HUMAN	STANDARD;	PRT;	109 AA.	
AC	P83593;				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Ig kappa chain V-IV region STH (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Abdominal adipose tissue;				
RX	MEDLINE=98249779; PubMed=9588180; DOI=10.1006/brc.1998.8515;				
RA	Olsen K.E., Sletten K., Westermarck P.;				
RT	"Extended analysis of AL-amyloid protein from abdominal wall				
RT	subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";				
RL	Biochem. Biophys. Res. Commun. 245:713-716(1998).				
CC	-I- FUNCTION: May play an important role in fibrillogenesis.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Direct protein sequencing; Immunoglobulin V region.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 40				
FT	DOMAIN 41 55				
FT	DOMAIN 56 62				
FT	DOMAIN 63 94				
FT	DOMAIN 95 101				
FT	DOMAIN 102 109				
FT	DISULFID 23 94				
FT	UNSURE 23 23				
FT	UNSURE 94 94				
FT	NON TER 109 109				
SQ	SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 38; DB 1; Length 109;					
Matches 7; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 WASTRES 7				
Db	56 WASTRES 62				
RESULT 2					
ID	KV4A_HUMAN	STANDARD;	PRT;	114 AA.	
AC	P01625;				
DT	21-JUL-1986 (Rel. 01, Created)				



```

DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE Ig kappa chain V-IV region len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1EEQ; X-ray; A/B=1-114.
DR PDB; 1EEU; X-ray; A/B=1-114.
DR PDB; 1EFQ; X-ray; A=1-114.
DR PDB; 1EK3; X-ray; A/B=1-114.
DR PDB; 1LVE; X-ray; @=1-114.
DR PDB; 3LVE; X-ray; A=1-114.
DR PDB; 5LVE; X-ray; A=1-114.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
KV
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 40 Complementarity-determining-1.
FT DOMAIN 41 55 Framework-2.
FT DOMAIN 56 62 Complementarity-determining-2.
FT DOMAIN 63 94 Framework-3.
FT DOMAIN 95 101 Complementarity-determining-3.
FT DOMAIN 102 113 Framework-4.
FT DISULFID 23 94 By similarity.
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 32 35
FT STRAND 36 37
FT STRAND 39 44
FT STRAND 46 47
FT STRAND 51 55
FT STRAND 56 58
FT STRAND 59 60
FT STRAND 62 63
FT TURN 66 67
FT TURN 68 73
FT TURN 74 75
FT STRAND 76 81
FT STRAND 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. NO. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 3
KV40 HUMAN STANDARD; PRT; 121 AA.
ID KV40 HUMAN
AC P063I2;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -I- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
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CC -----
DR EMBL; Z00023; CAA77318.1; -.
DR PIR; A01902; K4HU.
DR HSSP; P01625; 1LVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
KV
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DOMAIN 115 121 Framework-3.
FT DISULFID 43 114 By similarity.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. NO. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 76 WASTRES 82

RESULT 4
KV4B HUMAN STANDARD; PRT; 133 AA.
ID KV4B HUMAN

```

```
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC -----
CC EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJI.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-IV region JI.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 133;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 76 WASTRES 82

RESULT 5
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID KV4C_HUMAN
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X02990; CAA26733.1; -.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 121 Framework-4.
FT DOMAIN 122 133 Complementarity-determining-3.
FT DISULFID 43 114 Framework-4.
FT NON_TER 134 134 By similarity.
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 134;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 76 WASTRES 82

RESULT 6
Q9NP29 PRELIMINARY; PRT; 130 AA.
ID Q9NP29;
AC Q9NP29;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Microfibrillar protein 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96354815; PubMed=8753791; DOI=10.1006/bbrc.1996.1202;
RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;
RT "Two hypothetical proteins of human aortic adventitia, with Ig kappa,
RT collagenous, and aromatic-rich motifs.";
RL Biochem. Biophys. Res. Commun. 225:500-504(1996).
RN [2]
RP SEQUENCE FROM N.A.
```

RX MEDLINE=97367690; PubMed=9224393; DOI=10.1006/jbre.1997.5030;  
RA Ozsvath K.J., Hirose H., Xia S., Chew D., Knoetgen J. III,  
RA Tilson M.D.;  
RT "Expression of two novel recombinant proteins from aortic adventitia  
RT (kappafibs) sharing amino acid sequences with cytomegalovirus.";  
RL J. Surg. Res. 69:277-282(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF206020; AAF62402.1; -.  
DR HSSP; P01625; 1LVE.  
DR InterPro; IPR007110; Ig-like.  
FT NON\_TER 130 130  
SQ SEQUENCE 130 AA; 14128 MW; 51275185ACC6FA1E CRC64;  
  
Query Match 92.1%; Score 35; DB 2; Length 130;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
|||||:  
Db 76 WASTRDS 82

## RESULT 7

Q6G2K3 PRELIMINARY; PRT; 934 AA.

ID Q6G2K3 AC Q6G2K3; PRT; 934 AA.  
AC Q6G2K3; PRELIMINARY; PRT; 934 AA.  
DT 05-JUL-2004 (TtEMBLrel. 27, Created)  
DT 05-JUL-2004 (TtEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TtEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=BH11960;  
OS Bartonella henselae (Rochalimaea henselae).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bartonellaceae; Bartonella.  
OX NCBI\_TaxID=38323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 49882 / Houston 1;  
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;  
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,  
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,  
RA La Scola B., Holmberg M., Andersson S.G.E.;  
RT "The louse-borne human pathogen Bartonella quintana is a genomic  
RT derivative of the zoonotic agent Bartonella henselae.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).  
RL EMBL; BX897699; CAF27979.1; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 934 AA; 104092 MW; 238F0F60D2D5BF19 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 934;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6  
|||||:  
Db 98 WASTRE 103

## RESULT 8

Q8PL66 PRELIMINARY; PRT; 980 AA.

ID Q8PL66 AC Q8PL66; PRT; 980 AA.  
AC Q8PL66; PRELIMINARY; PRT; 980 AA.  
DT 01-OCT-2002 (TtEMBLrel. 22, Created)  
DT 01-OCT-2002 (TtEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TtEMBLrel. 26, Last annotation update)  
DE GGDEF family protein.  
GN OrderedLocustNames=XAC1940;  
OS Xanthomonas axonopodis (pv. citri).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.

OX NCBI\_TaxID=92829;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=306 / ATCC 13902 / XV 101;  
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
RA da Silva A.C.R., Ferro J.A., Rehnach F.C., Farah C.S., Furlan L.R.,  
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,  
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,  
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,  
RA Setubal J.C., Kitajima J.P.;  
RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
RT host specificities.";  
RL Nature 417:459-463(2002).  
RL EMBL; AE011829; AAM36802.1; -.  
DR InterPro; IPR000160; GGDEF.  
DR InterPro; IPR01110; Reg\_prop.  
DR InterPro; IPR01123; Y\_Y\_Y.  
DR Pfam; PF00990; GGDEF; 1.  
DR Pfam; PF07494; Reg\_prop; 10.  
DR Pfam; PF07495; Y\_Y\_Y; 1.  
DR SMART; SM00267; DUF1; 1.  
DR TIGRFAMs; TIGR00254; GGDEF; 1.  
DR PROSITE; PS50887; GGDEF; 1.  
KW Complete proteome.  
SQ SEQUENCE 980 AA; 107940 MW; 47179C81E6DCE442 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 980;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6  
|||||:  
Db 492 WASTRE 497

## RESULT 9

O6PJUS PRELIMINARY; PRT; 266 AA.

ID O6PJUS AC O6PJUS; PRT; 266 AA.  
AC O6PJUS; PRELIMINARY; PRT; 266 AA.  
DT 05-JUL-2004 (TtEMBLrel. 27, Created)  
DT 05-JUL-2004 (TtEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TtEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

```
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boufiard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011643; AAH11643.1; -.
KW Hypothetical protein.
SQ SEQUENCE 266 AA; 29322 MW; 5DE33CA2D1AD11A4 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 266;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 249 WASNRES 255

RESULT 10
Q8TFZ3 PRELIMINARY; PRT; 1317 AA.
ID Q8TFZ3;
AC Q8TFZ3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AfA35910.09C;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;
RA Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M.,
RA Foster N., Fraser A., Harris D., Larke N., Murphy L., Humphray S.,
RA O'Neil S., Perte M., Price C., Rabinowitsch E., Rajandream M-A.,
RA Salzberg S., Saunders D., Seegar K., Sharp S., Warren T.,
RA Denning D.W., Barrell B., Hall N.;
RT "Insight into the genome of Aspergillus fumigatus: analysis of a 922
RT kb region encompassing the nitrate assimilation gene cluster.";
RL Fungal Genet. Biol. 41:443-453(2004).
CC -1- SIMILARITY: Contains 3 WD repeats.
DR EMBL; BX649606; CAD29602.1; -.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 3.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 1317 AA; 148645 MW; 0DC4B0BD149A45DE CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 1317;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 979 WASARES 985

RESULT 11
Q915J7 PRELIMINARY; PRT; 347 AA.
ID Q915J7;
AC Q915J7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
```

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DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PA0732;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-D.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004508; AAG04121.1; -.
DR PIR; D83554; D83554.
DR InterPro; IPR005490; ErfK_Ybis_Yhng.
DR Pfam; PF03734; ErfK_Ybis_Yhng; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 347 AA; 37161 MW; 264E4DC064290CC3 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 318 WASTRDT 324

RESULT 12
Q7XUI8 PRELIMINARY; PRT; 458 AA.
ID Q7XUI8;
AC Q7XUI8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE OSJNB0103108.17 protein.
Name=OSJNB0103108.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL606695; CAD41278.2; -.
DR Gramene; Q7XUI8; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
```



```
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR01245; Tyr_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 458 AA; 49421 MW; 754DF9A9E23F7FEF8 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 2; Length 458;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WASTRES 7
Db 59 WASTRPS 65

RESULT 13
SYM_NEIMA STANDARD; PRT; 685 AA.
ID -SYM_NEIMA
AC Q9JWP0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (MetRS).
GN Name=metG; Ordered locus names=NMA0275;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(Met) aminoacylation (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family. MetG subfamily 1.
CC -!- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL162752; CAB83583.1; -.
DR PIR; G82022; G82022.
```

```
DR HSSP; P00959; 1MEA.
DR HAMAP; MF_00098; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR008224; MetRS_dimerising.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1i.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA_bind.
DR InterPro; IPR009080; tRNAsyn_1a_bind.
DR Pfam; PF00133; tRNA-synt_1.
DR Pfam; PF01588; tRNA_bind_1.
DR PIRSF; PIRSF001528; MetRS_dimerising; 1.
DR PRINTS; PR01041; TRNASYNTHMET.
DR TIGRFAMS; TIGR00398; metG; 1.
DR TIGRFAMS; TIGR00399; metG_Cterm; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
DR PROSITE; PS50886; TRBD; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Metal-binding; Protein biosynthesis; RNA-binding; tRNA-binding; Zinc.
FT SITE 12 22 "HIGH" region.
FT SITE 339 343 "KMSKS" region.
FT DOMAIN 582 685 tRNA-binding.
FT METAL 143 143 Zinc (By similarity).
FT METAL 146 146 Zinc (By similarity).
FT METAL 156 156 Zinc (By similarity).
FT METAL 159 159 Zinc (By similarity).
FT BINDING 342 342 ATP (By similarity).
SQ SEQUENCE 685 AA; 76984 MW; 07FD45915ED3BEF3 CRC64;
```

```
Query Match
Best Local Similarity 84.2%; Score 32; DB 1; Length 685;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 WASTRES 7
Db 520 WANTRET 526
```

```
RESULT 14
O7QYCI PRELIMINARY; PRT; 71 AA.
ID O7QYCI
AC O7QYCI;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE GUP_387_11136_11351.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB0100052; EAA40034.1; -.
SQ SEQUENCE 71 AA; 8127 MW; 0374829B52C40EE3 CRC64;
```

```
Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 71;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 WASTRES 7
Db 65 WASSRQS 71
```

RESULT 15



Q9N5V2  
ID Q9N5V2 PRELIMINARY; PRT; 171 AA.  
AC Q9N5V2;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Hypothetical protein CC8.1;  
GN Name=CC8.1; ORFNames=CC8.1;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Kemp K., Le T.T.;  
RT "The sequence of C. elegans cosmid CC8.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.H.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RG WormBase Consortium;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC006626; AAF39788.1; -.  
DR Intact; Q9N5V2; -.  
DR WormBase; WBGene00016986; CC8.1.  
DR WormPep; CC8.1; CE20616.  
KW Hypothetical protein.  
SQ SEQUENCE 171 AA; 17643 MW; 03AD96B9A627CFD CRC64;

Db 122 WATTRE 127  
Search completed: March 1, 2005, 17:43:19  
Job time : 47.3385 secs

Query Match 81.6%; Score 31; DB 2; Length 171;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRE 6

1110 PAGE BLANK (USPTO)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 59.8154 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-20  
Perfect score: 41  
Sequence: 1 KQSYNLRT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	8	3	AAV32228	Aay32228 G-CSF ago
2	41	100.0	114	2	AAV06830	Aay06830 Mouse Mab
3	41	100.0	148	1	AAP93078	Aap93078 Light cha
4	41	100.0	219	2	AAR44495	Aar44495 Sequence
5	41	100.0	265	2	AAR52864	Aar52864 Glycophor
6	36	87.8	84	2	AAW14491	Aaw14491 Monoclonal
7	36	87.8	84	2	AAR99878	Aar99878 Monoclonal
8	35	85.4	8	2	AAR76084	Aar76084 Mab 55.1
9	35	85.4	219	2	AAR76086	Aar76086 Mab 55.1
10	35	85.4	239	2	AAR76087	Aar76087 Mab 55.1
11	35	85.4	288	2	AAW82743	Aaw82743 Fusion pr
12	35	85.4	673	2	AAW82742	Aaw82742 Plasmid p
13	34	82.9	249	2	AAW60770	Aaw60770 Single ch
14	33	80.5	8	2	AAW70910	Aaw70910 CDR3 of t
15	33	80.5	18	2	AAW70916	Aaw70916 Peptide p
16	33	80.5	110	2	AAW56520	Aaw56520 Anti-DNA
17	33	80.5	110	2	AAW56517	Aaw56517 H221 anti
18	32	78.0	166	4	AAU71926	Aau71926 Human bon
19	32	78.0	318	5	AAE20107	Aae20107 Lactobaci
20	32	78.0	453	5	ABB09487	Abb09487 AMEPV CPD
21	31	75.6	37	5	AAE23239	Aae23239 Streptoco
22	31	75.6	114	2	AAV06831	Aay06831 Mouse Mab
23	31	75.6	161	7	ADC95923	Adc95923 E. faeciu
24	31	75.6	283	2	AAW93214	Aaw93214 A. gelati
25	31	75.6	370	7	ADF69092	Adf69092 Human MP5

26	31	75.6	422	6	ABU41136	Abu41136 Protein e
27	31	75.6	424	7	ADF06925	Adf06925 Bacterial
28	31	75.6	437	4	AAG62618	Aag62618 Petunia z
29	31	75.6	437	4	AAG64524	Aag64524 P. hybrid
30	31	75.6	437	7	ADD02815	Add02815 Petunia h
31	31	75.6	437	8	ADF38736	Adf38736 Petunia x
32	31	75.6	539	8	ADL00081	Adl00081 Streptoco
33	31	75.6	541	5	AAE23235	Aae23235 Streptoco
34	31	75.6	542	8	ADL00082	Adl00082 Streptoco
35	31	75.6	542	8	ADL00077	Adl00077 Streptoco
36	31	75.6	542	8	ADL00079	Adl00079 Streptoco
37	31	75.6	542	8	ADL00083	Adl00083 Streptoco
38	31	75.6	542	8	ADL00084	Adl00084 Streptoco
39	31	75.6	542	8	ADL00080	Adl00080 Streptoco
40	31	75.6	542	8	ADL00085	Adl00085 Streptoco
41	31	75.6	542	8	ADL00078	Adl00078 Streptoco
42	31	75.6	542	8	ADL00086	Adl00086 Streptoco
43	31	75.6	543	5	ABP29881	Abp29881 Streptoco
44	31	75.6	543	8	ADL00076	Adl00076 Streptoco
45	31	75.6	543	8	ADO10465	Ado10465 Group B S

ALIGNMENTS

RESULT 1	AAV32228	standard; peptide; 8 AA.
ID	AAV32228;	
AC	AAV32228;	
DT	15-FEB-2000	(first entry)
DE	G-CSF agonist antibody mAb163-93	light chain variable region CDR3.
KW	Granulocyte colony stimulating factor receptor; G-CSF; mouse; monoclonal antibody; agonist; screening; neutropenia; therapy; complementarity determining region; CDR; mAb163-93.	
OS	Mus musculus.	
PN	WO9955735-A1.	
PD	04-NOV-1999.	
PF	30-APR-1999;	99WO-US009466.
PR	30-APR-1998;	98US-Q083575P.
PA	(TANO-) TANOX INC.	
PI	Ni B, Sun BNC, Sun CRY;	
DR	WPI; 2000-052805/04.	
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic cell lineage progenitors.	
PS	Claim 13; Page 30; 64pp; English.	
CC	The present sequence represents complementarity determining region 3 (CDR3) of the light chain variable region of murine monoclonal antibody mAb163-93. This antibody is an example of an agonist molecule that specifically binds to or interacts with human granulocyte colony stimulating factor (G-CSF) receptor to stimulate cell proliferation and differentiation, especially by dimerising the receptor or activating phosphorylation of kinases associated with the receptor. Agonist antibodies can be used to stimulate proliferation of G-CSF-dependent cells, e.g. to differentiate leading to a repopulation of neutrophilic granulocyte lineage cells, especially to treat neutropenia (claimed). They can also be used to detect human G-CSF receptor immunologically	
XX	Sequence 8 AA;	
SO		

Query Match 100.0%; Score 41; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
|||  
Db 1 KQSYNLRT 8

RESULT 2  
AAV06830  
ID AAY06830 standard; protein; 114 AA.

XX AAY06830;  
AC AAY06830;  
XX 25-JUN-1999 (first entry)  
DT 25-JUN-1999 (first entry)  
XX Mouse Mab 6A4 light chain variable region.  
DE Rolling template; nucleic acid synthesis; polynucleotide polymerase;  
KW gene production; primer; monoclonal antibody; 6A4; 88.  
XX Mus sp.  
OS WO9914370-A1.  
XX 25-MAR-1999.  
PD 15-SEP-1998; 98WO-US019157.  
PF 15-SEP-1997; 97US-00929856.  
XX 15-SEP-1997; 97US-00929856.  
PR (HIAT/) HIATT A C.  
PA (ROSE/) ROSE F D.  
XX Hiatt AC, Rose FD;  
PI WPI; 1999-244045/20.  
XX N-PSDB; AAX34465.  
DR  
XX  
PT Producing specific polynucleotides using rolling templates.

PS Example 6; Page 75; 109pp; English.

XX The invention relates to a method for producing polynucleotides having a  
CC defined sequence using rolling templates that successively add  
CC nucleotides (nts) to a longer primer strand. The method comprises: (i)  
CC incubating, under annealing conditions, a primer and a template that has  
CC a 5'-region not complementary to the primer, a 3'-region complementary to  
CC the 3'-end of primer and a non-reactive 3'-terminus, with the template  
CC being shorter than the primer; (ii) reacting the primer with at least one  
CC nt in presence of a template-dependent polynucleotide polymerase to  
CC extend it by at least one nt (complementary to the 5'-region of template)  
CC at its 3'-end; (iii) separating the template and the extended primer; and  
CC (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize  
CC the desired polynucleotide. The method is especially used to produce  
CC genes or their segments. The method provides fast, accurate, inexpensive  
CC synthesis of RNA or DNA and is more efficient than chemical coupling  
CC processes. It has higher specificity and eliminates the need for  
CC deprotection. The products can be cloned directly. The method avoids  
CC problems of waste disposal and includes an inherent editing effect  
CC (failure sequences will not be extended further in subsequent rounds) so  
CC that purification of the end product is facilitated. Synthesis may take  
CC place on a vector, simplifying cloning and sequences with codon usage  
CC optimized for a particular host can be prepared. This represents the  
CC amino acid sequence of the light chain variable region of the mouse  
CC monoclonal antibody (Mab) 6A4, synthesised by the method of the invention  
XX  
SQ Sequence 114 AA;

Query Match 100.0%; Score 41; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KQSYNLRT 8  
|||  
Db 95 KQSYNLRT 102

RESULT 3  
AAP93078  
ID AAP93078 standard; peptide; 148 AA.

XX AAP93078;  
AC AAP93078;  
XX 25-MAR-2003 (revised)  
DT 31-OCT-2002 (revised)  
DT 14-MAR-1990 (first entry)  
XX light chain of monoclonal antibody 6A4.  
DE Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.

XX Unidentified.  
OS EP338395-A.  
XX 25-OCT-1989.  
PD 12-APR-1989; 89EP-00106463.  
PF 19-APR-1988; 88DE-03813023.  
XX (BEHW ) BEHRINGWERKE AG.

PA Domdey H, Marget M, Vonspecht B;  
XX WPI; 1989-310861/43.  
DR N-PSDB; AAN91663.  
XX  
PT Monoclonal antibody to pseudomonas aeruginosa - and DNA coding for  
PT variable antibody regions.  
XX  
PS Claim 1; Page 6; 7pp; German.

XX The peptide is encoded by the light chain of monoclonal antibody 6A4. 6A4  
CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.  
CC It is used for therapy and diagnosis of infection, and as a carrier for  
CC drugs. The antibody is IgG2a subclass. (Updated on 31-OCT-2002 to add  
CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated  
CC on 25-MAR-2003 to correct PI field.)  
XX  
SQ Sequence 148 AA;

Query Match 100.0%; Score 41; DB 1; Length 148;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
|||  
Db 115 KQSYNLRT 122

RESULT 4  
AAR44495  
ID AAR44495 standard; protein; 219 AA.

XX AAR44495;  
AC AAR44495;  
XX 25-MAR-2003 (revised)  
DT 26-MAY-1994 (first entry)  
XX  
DE Sequence of the immunoglobulin IgG (1C3/86) kappa chain derived from  
DE clone gammal.1.1a and augmented using PCR.  
XX

KM Particle-binding antibody fragment; kappa chain;  
KW monoclonal cell line 1C3/86; anti-erythrocyte IgGs.  
XX  
OS Synthetic.  
XX  
PN WO9324630-A1.  
XX  
PD 09-DEC-1993.  
XX  
PF 19-MAY-1993; 93WO-AU000228.  
XX  
PR 22-MAY-1992; 92AU-00002551.  
XX  
PA (AGEN-) AGEN LTD.  
XX  
PI Lilley GG, Hudson PJ, Hillyard CJ;  
XX  
DR WPI; 1993-405821/50.  
DR N-PSDB; AAQ53430.  
XX  
PT Bifunctional recombinant protein - contains particle and analyte binding  
PT moieties, used in agglutination assays pref. on whole blood.  
XX  
PS Example; Fig 2; 42pp; English.  
XX  
CC mRNA was prepd. from monoclonal antibody cell line (1C3/86) which prods  
CC anti-erythrocyte IgGs which bind to RBCs. ds-cDNA was prepd. and cloned  
CC into lambda-gt10 arms and packaged into a phage library. The heavy chain  
CC clone gamma-M/1.1 and the light chain clone ph76-kappa-10 were used to  
CC source ds-DNA inserts for the screening of the gt10 library. Positive  
CC clones were amplified, and the positive insert cDNA subcloned into pUC18.  
CC As a result a near full-length gamma clone (gamma-1.1.1a) was identified,  
CC the nucleotide sequence was determined and from this the protein sequence  
CC deduced (AAQ53429/R4494). The sequences of a partial kappa clone (kappa-  
CC 4Acl) which encoded the 3' end of the variable domain and full constant  
CC domain were determined in a similar fashion. To determine the sequence  
CC the 1C3/86 kappa light chain at the 5' end, a mixed N-terminal sequence  
CC was determined from the intact 1C3/86 Ig and together with the sequence  
CC from a gamma heavy chain clone used to determine the N-terminus of the  
CC variable region of the kappa light chain. A coding sequence for this  
CC amino acid sequence was compiled and PCR amplified using the redundant  
CC forward (sense) primer N960 and the reverse (antisense) primer N852)  
CC which was based on the kappa constant region beginning at nucleotide 337  
CC (see AAQ53430). The sequences derived from the PCR and gt10 library  
CC enabled the compilation of the sequence in AAQ53430. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 219 AA;  
Query Match 100.0%; Score 41; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KQSYNLR 8  
DB 95 KQSYNLR 102  
RESULT 5  
AAAR52864  
ID AAR52864 standard; protein; 265 AA.  
XX  
AC AAR52864;  
XX  
DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 09-SEP-1994 (first entry)  
XX  
DE Glycophorin antibody 1C3 scFv.  
XX  
KW Glycophorin; antibody 1C3; target binding polypeptide; PCR;  
KW polymerase chain reaction; primer; scFv; single chain antibody;  
KW phagemid pHFA; vector; antibody engineering; humanized antibody.

XX  
OS Unidentified.  
XX  
PN WO9407921-A1.  
XX  
PD 14-APR-1994.  
XX  
PF 24-SEP-1993; 93WO-AU000491.  
XX  
PR 25-SEP-1992; 92AU-00004973.  
XX  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
PI Hudson PJ, Lah M, Kortt A, Irving RA, Atwell JL, Malby RL;  
PI Power BE, Colman PM;  
XX  
DR WPI; 1994-135515/16.  
DR N-PSDB; AAQ62956.  
XX  
PT New target-binding polypeptide(s) used for diagnosis, etc. - having a  
PT stable core polypeptide region with at least one target-binding region  
PT covalently attached, opt. mutated to alter specificity, etc.  
XX  
PS Disclosure; Page 40; 67pp; English.  
XX  
CC PCR primers N2034 (AAQ62947) and N2035 (AAQ62948) were used with anti-  
CC glycophorin 1C3 antibody template DNA in a PCR to produce a 1C3 product  
CC of 3'-VH sequence juxtaposed to 5'-VL sequence flanked by BstEII and NotI  
CC sites. Products were ligated with vector pHFA containing a 1C3 scFv  
CC sequence, and expressed in Escherichia coli TGI. The DNA sequence of the  
CC linkerless 1C3 scFv in pHFA is given in AAQ62956 (encoding protein  
CC AAR52864). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-  
CC MAR-2003 to correct FI field.) (Updated on 27-AUG-2003 to correct OS  
CC field.)  
XX  
SQ Sequence 265 AA;  
Query Match 100.0%; Score 41; DB 2; Length 265;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KQSYNLR 8  
DB 236 KQSYNLR 243  
RESULT 6  
AAAW14491  
ID AAW14491 standard; protein; 84 AA.  
XX  
AC AAW14491;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JAN-1997 (first entry)  
XX  
DE Monoclonal antibody D VK.  
XX  
KW heavy; light chain; monoclonal antibody; antigen 3; marker; melanoma;  
KW permanent human tumour cell line; tumour-associated antigen; epitope;  
KW gastrointestinal tumour; pancreatic carcinoma; diagnostic; therapeutic;  
KW antigen 11; Vibrio cholera; neuraminidase-resistant; ganglioside GD2.  
XX  
OS Synthetic.  
XX  
PN EP727436-A1.  
XX  
PD 21-AUG-1996.  
XX  
PF 21-MAR-1990; 96EP-00100443.  
XX  
PR 24-MAR-1989; 89DE-03909799.  
PR 21-MAR-1990; 90EP-00105322.  
XX



PA (BEHW ) BEHRINGWERKE AG.  
XX  
PI Bosslet K, Seemann G, Sedlacek H, Auerbach B;  
XX  
DR WPI; 1996-372836/38.  
DR N-PSDB; AAT63508.  
XX  
PT Monoclonal antibody to tumour-associated antigen - useful as  
PT gastrointestinal tumour marker.  
XX  
PS Disclosure; Page 14; 19pp; German.  
XX  
CC AAW14490-91 are the heavy and light chains (respectively) of monoclonal  
CC antibody (Mab) D. Mab D recognises Vibrio cholera neuraminidase-resistant  
CC epitope of ganglioside GD2, from a human melanoma cell line. Mabs A, B  
CC and C (see AAW14484-89) are mentioned in the specification, but are not  
CC part of the claims. Mabs A and B recognise antigens 3 and 11 resp., of a  
CC permanent human tumour cell line. Mab C also recognises an epitope of a  
CC tumour-associated antigen. These antigens occur at high concns. in the  
CC serum of patients with gastrointestinal tumours, e.g. pancreatic  
CC carcinoma, and are thus useful as tumour markers for diagnostic or  
CC therapeutic purposes. (Updated on 25-MAR-2003 to correct PF field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)  
CC  
XX  
SQ Sequence 84 AA;  
  
Query Match 87.8%; Score 36; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KQSYNLR 7  
|||  
67 KQSYNLR 73  
DB  
  
RESULT 7  
AAR99878  
ID AAR99878 standard; protein; 84 AA.  
XX  
AC AAR99878;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JAN-1997 (first entry)  
XX  
DE Monoclonal antibody D VK.  
XX  
KW Monoclonal antibody; Mab; epitope; tumour-associated antigen; marker;  
KW antigen.  
XX  
OS Synthetic.  
XX  
PN EP727435-A1.  
XX  
PD 21-AUG-1996.  
XX  
PF 21-MAR-1990; 96EP-00100442.  
XX  
PR 24-MAR-1989; 89DE-03909799.  
PR 21-MAR-1990; 90EP-00105322.  
XX  
PA (BEHW ) BEHRINGWERKE AG.  
XX  
PI Bosslet K, Seemann G, Sedlacek H, Auerbach B;  
XX  
DR WPI; 1996-372835/38.  
DR N-PSDB; AAT36666.  
XX  
PT Monoclonal antibody to tumour-associated antigen - useful as  
PT gastrointestinal tumour marker.  
XX  
PS Disclosure; Page 14; 19pp; German.  
XX  
CC Mab C (AAT36659-T36660) is a monoclonal antibody that recognises an

CC epitope of a tumour-associated antigen occurring at high concn. in the  
CC serum of patients with gastrointestinal tumours, e.g. pancreatic  
CC carcinoma, and is thus useful as a tumour marker for diagnostic or  
CC therapeutic purposes. Mabs A, B and D are mentioned in the specification,  
CC but are not part of the claims. Mab A (AAT36661-T36662) recognises  
CC antigen 3 of permanent human tumour cell line. Mab B (AAT36663-T36664)  
CC recognises antigen 11 of permanent human tumour cell line. Mab D  
CC (AAT36665-T36666) recognises a Vibrio cholera neuraminidase-resistant  
CC epitope of ganglioside GD2, from a human melanoma cell line. (Updated on  
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR  
CC field.)  
XX  
SQ Sequence 84 AA;  
  
Query Match 87.8%; Score 36; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KQSYNLR 7  
|||  
67 KQSYNLR 73  
DB  
  
RESULT 8  
AAR76084  
ID AAR76084 standard; peptide; 8 AA.  
XX  
AC AAR76084;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX  
DE Mab 55.1 light chain CDR3.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.  
XX  
OS Mus sp.  
XX  
PN WO9515382-A1.  
XX  
PD 08-JUN-1995.  
XX  
PF 29-NOV-1994; 94WO-GB002610.  
XX  
PR 03-DEC-1993; 93GB-00024819.  
PR 03-JUN-1994; 94GB-00011089.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;  
XX  
DR WPI; 1995-215262/28.  
XX  
PT Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.  
XX  
PS Claim 2; Page 97; 121pp; English.  
XX  
CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
CC of the heavy and light chains of Mab 55.1 (ECACC 93081901), which  
CC recognises the colorectal tumor-associated antigen CA55.1. It is  
CC optionally humanized and in the form F(ab')2, F(ab)', Fab, Fv, scFv or V-  
CC min, and is produced in transgenic animals or plants. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 8 AA;

Query Match 85.4%; Score 35; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KOSYNLRT 8  
Db 1 KOSYTLRT 8  
RESULT 9  
AAR76086  
ID AAR76086 standard; peptide; 219 AA.  
XX  
AC AAR76086;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX  
DE MAb 55.1 light chain.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.  
XX  
OS Mus sp.  
XX  
PN WO9515382-A1.  
XX  
PD 08-JUN-1995.  
XX  
PF 29-NOV-1994; 94WO-GB002610.  
XX  
PR 03-DEC-1993; 93GB-00024819.  
PR 03-JUN-1994; 94GB-00011089.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;  
XX  
DR WPI; 1995-215262/28.  
XX  
PT Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.  
XX  
PS Claim 3; Page 98; 121pp; English.  
XX  
CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
CC of the heavy (AAR76085) and light (AAR76086) chains of MAb 55.1 (ECACC  
CC 93081901), which recognises the colorectal tumor-associated antigen  
CC CA55.1. It is optionally humanized and in the form F(ab')<sub>2</sub>, Fab,  
CC Fv, scFv or V-min, and is produced in transgenic animals or plants.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 219 AA;  
Query Match 85.4%; Score 35; DB 2; Length 219;  
Best Local Similarity 87.5%; Pred. No. 55;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KOSYNLRT 8  
Db 95 KOSYTLRT 102  
RESULT 10  
AAR76087  
ID AAR76087 standard; protein; 239 AA.  
XX  
AC AAR76087;

XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX  
DE MAb 55.1 light chain.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..20 /label= sig\_peptide  
FT Protein 21..239 /label= Mat\_protein  
FT /note= "claim 3, page 98"  
XX  
PN WO9515382-A1.  
XX  
PD 08-JUN-1995.  
XX  
PF 29-NOV-1994; 94WO-GB002610.  
XX  
PR 03-DEC-1993; 93GB-00024819.  
PR 03-JUN-1994; 94GB-00011089.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
PI Blakey DC;  
XX  
DR WPI; 1995-215262/28.  
DR N-PSDB; AAQ94036.  
XX  
PT Antigen binding structures containing CDR's recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
PT and therapy of cancer.  
XX  
PS Disclosure; Fig 16; 121pp; English.  
XX  
CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
CC chains of 55.1 were isolated, and F(ab')<sub>2</sub>, Fab, Fv, scFv or V-min  
CC humanized 55.1 constructs have been expressed in myeloma cells and E.  
CC coli. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 239 AA;  
Query Match 85.4%; Score 35; DB 2; Length 239;  
Best Local Similarity 87.5%; Pred. No. 60;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KOSYNLRT 8  
Db 115 KOSYTLRT 122  
RESULT 11  
AAW82743  
ID AAW82743 standard; protein; 288 AA.  
XX  
AC AAW82743;  
XX  
DT 10-MAY-1999 (first entry)  
XX  
DE Fusion protein PNG4/55.1scFv/CPG2 R6/del EcoRI.  
XX  
KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
KW produg-converting enzyme; cell surface antigen; treatment; cancer;

KW inflammation; rheumatoid arthritis; antibody; prodrug therapy system.  
XX  
XX Synthetic.  
OS  
XX WO9851787-A2.  
PN  
XX 19-NOV-1998.  
PD  
XX 05-MAY-1998; 98WO-GB001294.  
PF  
XX 10-MAY-1997; 97GB-00009421.  
PR  
XX (ZENE ) ZENECA LTD.  
PA  
XX Emery SC, Blakey DC;  
PI  
XX WPI; 1999-059700/05.  
DR  
XX N-PSDB; AAV72064.  
DR  
XX  
PT New gene construct expressing conjugate of targeting agent and prodrug-  
PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
PT drug in vivo, especially for treatment of cancer.  
XX  
XX  
PS Example 15; Page 82; 100pp; English.  
XX  
CC This sequence is a used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
CC and (B) is directed to leave the cell for selective localisation at a  
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
CC site, then administration of (III) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme prodrug therapy  
CC system  
XX  
SQ Sequence 288 AA;

Query Match 85.4%; Score 35; DB 2; Length 288;  
Best Local Similarity 87.5%; Pred. No. 72;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLRT 8  
|||  
253 KQSYTLRT 260

RESULT 12

AAW82742  
ID AAW82742 standard; protein; 673 AA.

XX  
AC AAW82742;

XX  
DT 10-MAY-1999 (first entry)

XX  
DE Plasmid pMG4/55.lacFv/CPG2 R6 protein.

XX  
KW Conjugate; cell targeting; cytotoxic drug; prodrug-converting enzyme;  
KW cell surface antigen; treatment; cancer; inflammation; antibody;  
KW rheumatoid arthritis; prodrug therapy system.

XX  
OS Synthetic.

XX  
PN WO9851787-A2.

XX  
PD 19-NOV-1998.

XX  
PF 05-MAY-1998; 98WO-GB001294.

XX  
PR 10-MAY-1997; 97GB-00009421.

XX  
PA (ZENE ) ZENECA LTD.

XX  
PI Emery SC, Blakey DC;  
XX  
DR WPI; 1999-059700/05.  
DR  
XX N-PSDB; AAV72059.

PT New gene construct expressing conjugate of targeting agent and prodrug-  
PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
PT drug in vivo, especially for treatment of cancer.

XX  
PS Example 14; Page 78-79; 100pp; English.

XX  
CC This sequence is used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
CC and (B) is directed to leave the cell for selective localisation at a  
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
CC site, then administration of (III) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme prodrug therapy  
CC system  
XX  
SQ Sequence 673 AA;

Query Match 85.4%; Score 35; DB 2; Length 673;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLRT 8  
|||  
250 KQSYTLRT 257

RESULT 13

AAW60770  
ID AAW60770 standard; protein; 249 AA.

XX  
AC AAW60770;

XX  
DT 08-SEP-1998 (first entry)

XX  
DE Single chain antibody (ScFv) D3M that binds to mutant p53 proteins.

XX  
KW Single chain antibody; ScFv D3M; mouse; p53 protein; oligomerisation;

XX  
KW regulatory domain; p53 mutant; H273; W248; G281;

XX  
KW p53-dependent trans-activating activity; restoration;  
KW tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;  
KW cancer; re-stenosis; ss.

XX  
OS Mus sp.

XX  
PN WO9818825-A1.

XX  
PD 07-MAY-1998.

XX  
PF 27-OCT-1997; 97WO-FR001921.

XX  
PR 29-OCT-1996; 96FR-00013176.

XX  
PA (RHON ) RHONE-POULENC RORER SA.

XX  
PI Bracco L, Debussche L;

XX  
DR WPI; 1998-272140/24.

XX  
DR N-PSDB; AAV36237.

PT Restoring p53-dependent trans-activating activity to cell containing  
PT mutant p53 - by delivering single-chain antibody specific for the mutant,  
PT particularly for treatment of tumours.

PS Claim 5; Page 32; 54pp; French.

XX The present sequence represents a single chain antibody (ScFv) designated  
CC D3M. The antibody binds to an epitope present in the C-terminal region of  
CC the p53 protein that includes oligomerisation and regulatory domains,  
CC specifically between positions 320 and 393. ScFv D3M is directed against  
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is  
CC introduced into cells containing a mutant p53 protein, p53-dependent  
CC trans-activating activity is restored. ScFv D3M is specific for p53-  
CC mutants that have lost tumour-suppressing activity and are present in  
CC tumour cells. It is particularly used to treat hyper-proliferation  
CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
CC and to purify or detect p53

XX Sequence 249 AA;

Query Match 82.9%; Score 34; DB 2; Length 249;  
Best Local Similarity 87.5%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLRT 8  
Db 232 KQSYNLPT 239

RESULT 14  
AAW70910  
ID AAW70910 standard; peptide; 8 AA.

XX AAW70910;  
XX 14-OCT-1998 (first entry)

DE CDR3 of the light chain of monoclonal antibody RS-348.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
KM respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
KM viral infection; inhibit; fusion; protection; transcription;  
KM antiviral agent; prophylaxis; diagnosis; infection; contamination.

OS Synthetic.  
OS Mus sp.

PN FR2758331-A1.

XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-00000300.

XX 14-JAN-1997; 97FR-00000300.

PA (UYBO-) UNIV BOURGOGNE.

XX WPI; 1998-390320/34.

PT New peptide(s) recognising viral epitope with tropism to mucosa - useful  
PT for, e.g. diagnosing, preventing and treating viral infection(s).

PS Claim 8; Fig 3; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by antigen-  
CC antibody type reactions, at least 1 epitope of a pathogenic virus having  
CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR  
CC regions of monoclonal antibodies specific for respiratory syncytial virus  
CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies  
CC specific for site III or IV of the VP6 protein of rota virus (RV). The  
CC peptides can neutralise viral infections and may also inhibit fusion  
CC between infected and uninfected cells or cells and viruses. They provide  
CC passive or active protection and/or inhibit transcription of the virus,  
CC so are useful as antiviral agents or for prophylaxis, in human or  
CC veterinary medicine. The peptides can be labelled and used to diagnose  
CC infection or contamination by the virus. The peptides are particularly  
CC directed against RSV or RS but may also be used against papilloma, adeno,

CC entero, polio, influenza or immune deficiency viruses  
XX Sequence 8 AA;

Query Match 80.5%; Score 33; DB 2; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLRT 8  
Db 1 KQSYNLPT 8

RESULT 15  
AAW70916  
ID AAW70916 standard; peptide; 18 AA.

XX AAW70916;

DT 14-OCT-1998 (first entry)

DE Peptide PEP3L, homologous to light chain CDR3 of antibody RS-348.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
KM respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;  
KM viral infection; inhibit; fusion; protection; transcription;  
KM antiviral agent; prophylaxis; diagnosis; infection; contamination.

OS Synthetic.  
OS Mus sp.

PN FR2758331-A1.

XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-00000300.

XX 14-JAN-1997; 97FR-00000300.

PA (UYBO-) UNIV BOURGOGNE.

XX WPI; 1998-390320/34.

PT New peptide(s) recognising viral epitope with tropism to mucosa - useful  
PT for, e.g. diagnosing, preventing and treating viral infection(s).

PS Claim 8; Fig 5; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by antigen-  
CC antibody type reactions, at least 1 epitope of a pathogenic virus having  
CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR  
CC regions of monoclonal antibodies specific for respiratory syncytial virus  
CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies  
CC specific for site III or IV of the VP6 protein of rota virus (RV). The  
CC peptides can neutralise viral infections and may also inhibit fusion  
CC between infected and uninfected cells or cells and viruses. They provide  
CC passive or active protection and/or inhibit transcription of the virus,  
CC so are useful as antiviral agents or for prophylaxis, in human or  
CC veterinary medicine. The peptides can be labelled and used to diagnose  
CC infection or contamination by the virus. The peptides are particularly  
CC directed against RSV or RS but may also be used against papilloma, adeno,  
CC entero, polio, influenza or immune deficiency viruses

XX Sequence 18 AA;

Query Match 80.5%; Score 33; DB 2; Length 18;  
Best Local Similarity 87.5%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLRT 8  
Db 4 KQSYNLPT 11

Search completed: March 1, 2005, 17:36:10  
Job time : 61.8154 secs



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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 15.6308 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-20  
Perfect score: 41  
Sequence: 1 KOSYNLRT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	114	3	US-08-929-856-66 Sequence 66, Appl
2	41	100.0	265	2	US-08-403-853-16 Sequence 16, Appl
3	36	87.8	109	2	US-08-308-494A-23 Sequence 23, Appl
4	35	85.4	8	1	US-08-353-400-32 Sequence 32, Appl
5	35	85.4	219	1	US-08-353-400-34 Sequence 34, Appl
6	35	85.4	239	1	US-08-353-400-37 Sequence 37, Appl
7	35	85.4	288	3	US-09-423-439-38 Sequence 38, Appl
8	35	85.4	673	3	US-09-423-439-32 Sequence 32, Appl
9	33	80.5	110	3	US-08-957-001B-5 Sequence 5, Appl
10	33	80.5	110	3	US-08-957-001B-24 Sequence 24, Appl
11	33	80.5	110	3	US-09-496-301-5 Sequence 24, Appl
12	33	80.5	110	3	US-09-496-301-24 Sequence 24, Appl
13	31	75.6	114	3	US-08-929-856-189 Sequence 189, Appl
14	31	75.6	161	4	US-09-107-532A-5550 Sequence 5550, Ap
15	31	75.6	424	4	US-09-543-681A-7210 Sequence 7210, Ap
16	31	75.6	585	2	US-08-867-941-21 Sequence 21, Appl
17	31	75.6	585	3	US-09-074-658-21 Sequence 21, Appl
18	31	75.6	753	2	US-08-867-941-20 Sequence 20, Appl
19	31	75.6	753	3	US-09-074-658-20 Sequence 20, Appl
20	31	75.6	762	4	US-09-270-767-40204 Sequence 40204, A
21	31	75.6	762	4	US-09-270-767-55420 Sequence 55420, A
22	31	75.6	985	2	US-08-867-941-13 Sequence 13, Appl
23	31	75.6	985	2	US-08-867-941-17 Sequence 17, Appl
24	31	75.6	985	3	US-09-074-658-13 Sequence 13, Appl
25	31	75.6	985	3	US-09-074-658-17 Sequence 17, Appl
26	31	75.6	1000	2	US-08-867-941-12 Sequence 12, Appl
27	31	75.6	1000	2	US-08-867-941-16 Sequence 16, Appl

28	31	75.6	1000	3	US-09-074-658-12	Sequence 12, Appl
29	31	75.6	1000	3	US-09-074-658-16	Sequence 16, Appl
30	31	75.6	1003	4	US-09-540-236-2757	Sequence 2757, Ap
31	31	75.6	2432	3	US-09-074-658-15	Sequence 15, Appl
32	31	75.6	2439	3	US-09-074-658-11	Sequence 11, Appl
33	30	73.2	375	4	US-09-270-767-46302	Sequence 46302, A
34	30	73.2	401	4	US-09-270-767-56710	Sequence 56710, A
35	30	73.2	754	4	US-09-976-594-375	Sequence 41490, A
36	30	73.2	754	4	US-09-976-594-375	Sequence 375, App
37	30	73.2	760	4	US-09-949-016-11129	Sequence 11129, A
38	29	70.7	8	4	US-09-627-896B-20	Sequence 20, Appl
39	29	70.7	117	4	US-09-149-476-642	Sequence 642, App
40	29	70.7	132	4	US-09-627-896B-4	Sequence 4, Appl
41	29	70.7	132	4	US-09-627-896B-8	Sequence 8, Appl
42	29	70.7	239	4	US-09-627-896B-22	Sequence 22, Appl
43	29	70.7	431	3	US-09-381-681-3	Sequence 3, Appl
44	29	70.7	441	3	US-09-191-136-31	Sequence 31, Appl
45	29	70.7	616	4	US-09-248-796A-24217	Sequence 24217, A

ALIGNMENTS

RESULT 1  
US-08-929-856-66  
Sequence 66, Application US/08929856  
Patent No. 6136568  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Rose, Floyd  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
TITLE OF INVENTION: ROLLING TEMPLATES  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &  
ADDRESSEE: MENTILIK  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929, 856  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REGISTRATION NUMBER: 33, 071  
REFERENCE/DOCKET NUMBER: ROSE 3.0-057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-929-856-66

Query Match 100.0%; Score 41; DB 3; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KOSYNLRT 8  
Db 95 KOSYNLRT 102

```
RESULT 2
US-08-403-853-16
; Sequence 16, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-403-853-16

Query Match 100.0%; Score 41; DB 2; Length 265;
Best local Similarity 100.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KQSYNLRT 8
Db 236 KQSYNLRT 243

RESULT 3
US-08-308-494A-23
; Sequence 23, Application US/08308494A
; Patent No. 5959083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-308-494A-23

Query Match 87.8%; Score 36; DB 2; Length 109;
Best local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KQSYNLRT 7
Db 92 KQSYNLRT 98

RESULT 4
US-08-353-400-32
; Sequence 32, Application US/08353400
; Patent No. 566357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 32:
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-32

Query Match 85.4%; Score 35; DB 1; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 1 KOSYTLRT 8

RESULT 5

US-08-353-400-34  
Sequence 34, Application US/08353400  
Patent No. 5665357

GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-34

Query Match 85.4%; Score 35; DB 1; Length 219;  
Best Local Similarity 87.5%; Pred. No. 6.2;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 95 KOSYTLRT 102

RESULT 6

US-08-353-400-37  
Sequence 37, Application US/08353400  
Patent No. 5665357

GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400

FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-37

Query Match 85.4%; Score 35; DB 1; Length 239;  
Best Local Similarity 87.5%; Pred. No. 6.8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 115 KOSYTLRT 122

RESULT 7

US-09-423-439-38  
Sequence 38, Application US/09423439  
Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hillsbury Wintthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-423-439-38

Query Match 85.4%; Score 35; DB 3; Length 288;  
Best Local Similarity 87.5%; Pred. No. 8.3;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 253 KOSYTLRT 260

RESULT 8  
US-09-423-439-32  
; Sequence 32, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423,439  
; FILING DATE: 09-NO. 6339070-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32  
Query Match 85.4%; Score 35; DB 3; Length 673;  
Best Local Similarity 87.5%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KQSYNLR 8  
Db 250 KQSYTLRT 257  
RESULT 9  
US-08-957-001B-5  
; Sequence 5, Application US/08957001B  
; Patent No. 6228621  
; GENERAL INFORMATION:  
; APPLICANT: Williams, William V.  
; APPLICANT: Madaio, Michael  
; APPLICANT: Weiner, David B.  
; TITLE OF INVENTION: IMPROVED VACCINES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: windows  
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/957,001B  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/029,592  
; FILING DATE: 23-OCT-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: UPN-3303  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
US-08-957-001B-5  
Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KQSYNLR 8  
Db 95 KQSYTLRT 102  
RESULT 10  
US-08-957-001B-24  
; Sequence 24, Application US/08957001B  
; Patent No. 6228621  
; GENERAL INFORMATION:  
; APPLICANT: Williams, William V.  
; APPLICANT: Madaio, Michael  
; APPLICANT: Weiner, David B.  
; TITLE OF INVENTION: IMPROVED VACCINES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: windows  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/957,001B  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/029,592  
; FILING DATE: 23-OCT-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: UPN-3303  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-957-001B-24

Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 95 KOSYVLR 102

## RESULT 11

US-09-496-301-5  
Sequence 5, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madaio, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-09-496-301-5

Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 95 KOSYVLR 102

RESULT 12  
US-09-496-301-24  
Sequence 24, Application US/09496301  
Patent No. 6248565

GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madaio, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-496-301-24

Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 95 KOSYVLR 102

## RESULT 13

US-08-929-856-189  
Sequence 189, Application US/08929856  
Patent No. 6136568  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Rose, Floyd  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,856
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: ROSE 3.0-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-929-856-189

Query Match
Best Local Similarity 75.6%; Score 31; DB 3; Length 114;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYNLR 8
Db 97 SYNLR 102
```

## RESULT 14

```

; US-09-107-532A-5550
; Sequence 5550, Application US/09107532A
; Patent No. 6583275
```

## GENERAL INFORMATION:

```

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
```

```

; NUMBER OF SEQUENCES: 7310
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
```

```

; STREET: 100 Beaver Street
```

```

; CITY: Waltham
```

```

; STATE: Massachusetts
```

```

; COUNTRY: USA
```

```

; ZIP: 02354
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
```

```

; COMPUTER: PC
```

```

; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
```

```

; FILING DATE: 30-Jun-1998
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
```

```

; FILING DATE: 14 May 1998
```

```

; APPLICATION NUMBER: 60/051571
```

```

; FILING DATE: July 2, 1997
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
```

```

; REGISTRATION NUMBER: 40,489
```

```

; REFERENCE/DOCKET NUMBER: GTC-012
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
```

```

; TELEFAX: (781)893-8277
```

```

; INFORMATION FOR SEQ ID NO: 5550:
; SEQUENCE CHARACTERISTICS:
```

```

; LENGTH: 161 amino acids
```

```

; TYPE: amino acid
```

```

; TOPOLOGY: linear
```

```

; MOLECULE TYPE: protein
```

```

; HYPOTHETICAL: YES
```

```

; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1..161
; SEQUENCE DESCRIPTION: SEQ ID NO: 5550:
; US-09-107-532A-5550
```

```

Query Match
Best Local Similarity 75.6%; Score 31; DB 4; Length 161;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 KQSYNLR 8
Db 145 EQKYNLR 152
```

## RESULT 15

```

; US-09-543-681A-7210
; Sequence 7210, Application US/09543681A
; Patent No. 6605709
```

## GENERAL INFORMATION:

```

; APPLICANT: GARY BRETTON
```

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
```

```

; FILE REFERENCE: 2709.1002-001
```

```

; CURRENT APPLICATION NUMBER: US/09/543,681A
```

```

; PRIOR FILING DATE: 2000-04-05
```

```

; PRIOR APPLICATION NUMBER: US 60/128,706
```

```

; PRIOR FILING DATE: 1999-04-09
```

```

; NUMBER OF SEQ ID NOS: 8344
```

```

; SEQ ID NO 7210
```

```

; LENGTH: 424
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```

; TYPE: PRT
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```

; ORGANISM: Proteus mirabilis
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```

; US-09-543-681A-7210
```

```

Query Match
Best Local Similarity 75.6%; Score 31; DB 4; Length 424;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```

QY 1 KQSYNLR 8
Db 4 KTSYNLR 11
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```

Search completed: March 1, 2005, 17:46:58
Job time : 16.6308 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 42.8308 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-20  
Perfect score: 41  
Sequence: 1 KQSYNLRT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	8	US-10-071-962-20	Sequence 20, Appli
2	33	80.5	542	US-10-437-963-119563	Sequence 119563,
3	32	78.0	318	US-09-971-536-66	Sequence 66, Appli
4	32	78.0	453	US-10-706-635-14	Sequence 14, Appli
5	31	75.6	422	US-10-282-122A-69060	Sequence 69060, A
6	31	75.6	541	US-10-398-570-3	Sequence 3, Appli
7	31	75.6	546	US-10-091-007-2	Sequence 152957,
8	30	73.2	61	US-10-437-963-152957	Sequence 2, Appli
9	30	73.2	115	US-10-767-701-38209	Sequence 38209, A
10	30	73.2	126	US-09-864-408A-4176	Sequence 4176, Ap
11	30	73.2	235	US-10-437-963-145300	Sequence 145300,
12	30	73.2	237	US-10-472-928-1306	Sequence 1306, Ap
13	30	73.2	251	US-10-424-599-211909	Sequence 211909,

14	30	73.2	330	13	US-10-058-566-2	Sequence 2, Appli
15	30	73.2	330	16	US-10-437-963-142973	Sequence 142973,
16	30	73.2	428	15	US-10-425-114-50411	Sequence 50411, A
17	30	73.2	448	14	US-10-153-668-370	Sequence 370, App
18	30	73.2	683	16	US-10-620-669-20	Sequence 20, Appli
19	30	73.2	737	16	US-10-620-669-18	Sequence 18, Appli
20	30	73.2	754	14	US-10-153-668-254	Sequence 254, App
21	30	73.2	1720	16	US-10-437-963-114206	Sequence 114206,
22	29	70.7	8	9	US-09-249-011A-20	Sequence 20, Appli
23	29	70.7	83	15	US-10-424-599-157776	Sequence 157776,
24	29	70.7	117	10	US-09-809-391-642	Sequence 642, App
25	29	70.7	117	10	US-09-882-171-642	Sequence 642, App
26	29	70.7	117	15	US-10-164-861-642	Sequence 642, App
27	29	70.7	132	16	US-10-767-701-39825	Sequence 39825, A
28	29	70.7	132	9	US-09-249-011A-4	Sequence 4, Appli
29	29	70.7	132	9	US-09-249-011A-8	Sequence 8, Appli
30	29	70.7	239	9	US-09-249-011A-22	Sequence 22, Appli
31	29	70.7	302	15	US-10-425-114-46501	Sequence 46501, A
32	29	70.7	380	15	US-10-282-122A-54278	Sequence 54278, A
33	29	70.7	405	10	US-09-820-095-2	Sequence 2, Appli
34	29	70.7	429	15	US-10-282-122A-78300	Sequence 78300, A
35	29	70.7	431	10	US-09-820-095-4	Sequence 4, Appli
36	29	70.7	434	10	US-09-981-151A-66	Sequence 66, Appli
37	29	70.7	434	16	US-10-408-765A-1597	Sequence 1597, Ap
38	29	70.7	531	13	US-10-047-260-32	Sequence 32, Appli
39	29	70.7	547	10	US-09-977-418-4	Sequence 4, Appli
40	29	70.7	547	10	US-09-977-033A-4	Sequence 4, Appli
41	29	70.7	547	10	US-09-977-751C-4	Sequence 4, Appli
42	29	70.7	547	10	US-09-977-639A-4	Sequence 4, Appli
43	29	70.7	547	10	US-09-981-151A-24	Sequence 24, Appli
44	29	70.7	547	11	US-09-977-819B-4	Sequence 4, Appli
45	29	70.7	548	15	US-10-425-114-67811	Sequence 67811, A

ALIGNMENTS

RESULT 1  
US-10-071-962-20  
; Sequence 20, Application US/10071962  
; Publication No. US20030170237A1  
; GENERAL INFORMATION:  
; APPLICANT: BauFu Ni  
; APPLICANT: Bill N.C. Sun  
; APPLICANT: Cedilly R.Y. Sun  
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
; TITLE OF INVENTION: Screening Method Therefor  
; FILE REFERENCE: 98-3  
; CURRENT APPLICATION NUMBER: US/10/071,962  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US/09/303,155A  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/083,575  
; PRIOR FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-071-962-20

Query Match  
Best local Similarity 100.0%; Score 41; DB 14; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQSYNLRT 8  
Db 1 KQSYNLRT 8

RESULT 2  
US-10-437-963-119563

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; Sequence 119563, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 119563
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22769C.1.pep
US-10-437-963-119563
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Query Match      80.5%; Score 33; DB 16; Length 542;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 KQSYNLR 7
      :|||||
Db      457 RQSYNLR 463
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```
RESULT 3
US-09-971-536-66
; Sequence 66, Application US/09971536
; Patent No. US20020159976A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Blokeberg, Leonard
; APPLICANT: Lubbers, Mark
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul
; APPLICANT: Reid, Julian
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Methods
; TITLE OF INVENTION: Using Them
; FILE REFERENCE: 1043c2
; CURRENT APPLICATION NUMBER: US/09/971,536
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/NZ01/00160
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-971-536-66
```

```
Query Match      78.0%; Score 32; DB 9; Length 318;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 KQSYNLR 7
```

```
Db      73 KQKYNLR 79
```

```
RESULT 4
US-10-706-635-14
; Sequence 14, Application US/10706635
; Publication No. US20050014263A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Richard W.
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; TITLE OF INVENTION: Vertebrate Cells
; FILE REFERENCE: UF-221C1XCZ1
; CURRENT APPLICATION NUMBER: US/10/706,635
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/662,254
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Amsacta moorei entomopoxvirus
US-10-706-635-14
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```
Query Match      78.0%; Score 32; DB 17; Length 453;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY      1 KQSYNLR 8
      :|||||
Db      156 KQETNART 163
```

```
RESULT 5
US-10-282-122A-69060
; Sequence 69060, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69060
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-10-282-122A-69060
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Query Match      75.6%; Score 31; DB 15; Length 422;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 KQSYNLR 8
        |||||:
Db      2 KTSYNLRS 9
```

```
RESULT 6
US-10-398-570-3
; Sequence 3, Application US/10398570
; Publication No. US20040071730A1
; GENERAL INFORMATION:
; APPLICANT: SHIRE BIOCHEM INC.
; APPLICANT: MARTIN, Denis
; APPLICANT: RIOUX, Stephane
; APPLICANT: BOYER, Martine
; APPLICANT: HAMEL, Josee
; APPLICANT: BRODEUR, Bernard R.
; TITLE OF INVENTION: BVH-A2 and BVH-A3 ANTIGENS OF GBS
; FILE REFERENCE: 12806-23PCT
; CURRENT APPLICATION NUMBER: US/10/398,570
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/239,919
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Group B Streptococcus
; US-10-398-570-3
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Query Match      75.6%; Score 31; DB 15; Length 541;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 KQSYNLR 7
        |||||:
Db      8 KQSYSLR 14
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```
RESULT 7
US-10-091-007-2
; Sequence 2, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited
; APPLICANT: Le Page, Richard W F      Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
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```
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
; US-10-091-007-2
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Query Match      75.6%; Score 31; DB 14; Length 546;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KQSYNLR 7
        |||||:
Db      13 KQSYSLR 19
```

```
RESULT 8
US-10-437-963-152957
; Sequence 152957, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152957
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52957C.1.pep
; US-10-437-963-152957
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Query Match      73.2%; Score 30; DB 16; Length 61;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      2 QSYNLR 8
        |||||:
Db      4 QSYRLRT 10
```

```
RESULT 9
US-10-767-701-38209
; Sequence 38209, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: KOVALIC, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38209
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C50410_1.pep
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US-10-767-701-38209

Query Match  
Best Local Similarity 73.2%; Score 30; DB 16; Length 115;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
Db 73 KQSYQLNT 80

RESULT 10

US-09-864-408A-4176  
; Sequence 4176, Application US/09864408A  
; Publication No. US20040009474A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encc  
; FILE REFERENCE: 21402-012  
; CURRENT APPLICATION NUMBER: US/09/864,408A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/206,690  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 9068  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4176  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-864-408A-4176

Query Match  
Best Local Similarity 73.2%; Score 30; DB 11; Length 126;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
Db 92 KQSYQLNT 99

RESULT 11

US-10-437-963-145300  
; Sequence 145300, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 145300  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_46032C.1.pep  
US-10-437-963-145300

Query Match  
Best Local Similarity 73.2%; Score 30; DB 16; Length 235;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 224 KQSYNKHT 231

RESULT 12

US-10-472-928-1306  
; Sequence 1306, Application US/10472928  
; Publication No. US20050020813A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON spa  
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH  
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026926WO  
; CURRENT APPLICATION NUMBER: US/10/472,928  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: GB-0107658.7  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 4979  
; SOFTWARE: SeqMan99, version 1.03  
; SEQ ID NO 1306  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; OTHER INFORMATION: hypothetical protein  
; OTHER INFORMATION: Cellular location: membrane  
; OTHER INFORMATION: Similar to strain R6 sequence 15902655 (e-127)  
US-10-472-928-1306

Query Match  
Best Local Similarity 73.2%; Score 30; DB 17; Length 237;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
Db 79 KEKYNLQT 86

RESULT 13

US-10-424-599-211909  
; Sequence 211909, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 211909  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33380C.1.pep  
US-10-424-599-211909

Query Match  
Best Local Similarity 73.2%; Score 30; DB 15; Length 251;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 7  
Db 206 KQSYKLRT 212

RESULT 14

US-10-058-566-2  
; Sequence 2, Application US/10058566



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; Publication No. US20020183274A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMMELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; FILE REFERENCE: PHI 1147
; CURRENT APPLICATION NUMBER: US/10/058,566
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Zea mays
US-10-058-566-2
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Query Match      73.2%; Score 30; DB 13; Length 330;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 KQSYNLRT 8
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Db      288 KQSYQLNT 295
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RESULT 15
US-10-437-963-142973
; Sequence 142973, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142973
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43928C.1.pep
US-10-437-963-142973
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Query Match      73.2%; Score 30; DB 16; Length 330;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 KQSYNLRT 8
      |||||
Db      288 KQSYELNT 295
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Search completed: March 1, 2005, 17:52:52  
Job time : 43.8308 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 10.8308 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-20  
Perfect score: 41  
Sequence: 1 KOSYNLRT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	103	2	PH1050	Ig light chain V r
2	41	100.0	104	2	PH1101	Ig light chain V r
3	41	100.0	104	2	PH1102	Ig light chain V r
4	41	100.0	112	2	S41393	Ig kappa chain V r
5	41	100.0	112	2	S43103	Ig kappa chain V-J
6	41	100.0	133	2	PS0023	Ig kappa chain pre
7	34	82.9	97	2	A42575	Ig kappa chain V r
8	34	82.9	103	2	PH1047	Ig light chain V r
9	34	82.9	103	2	PH1051	Ig light chain V r
10	34	82.9	103	2	PH1052	Ig light chain V r
11	34	82.9	104	2	PH1103	Ig light chain V r
12	34	82.9	113	2	PT0408	Ig light chain V r
13	34	82.9	113	2	PT0407	Ig light chain V r
14	32	78.0	50	2	F97819	hypothetical prote
15	32	78.0	83	2	S53840	hypothetical prote
16	31	75.6	120	2	G33932	Ig kappa chain pre
17	31	75.6	549	2	H96944	arginine degradati
18	31	75.6	566	2	S39732	arginine/ornithine
19	31	75.6	667	2	C87236	probable zinc meta
20	31	75.6	761	1	S52769	subtilisin-like pr
21	30	73.2	104	2	PH1104	Ig light chain V r
22	30	73.2	173	2	A70133	hypothetical prote
23	30	73.2	237	2	A95081	hypothetical prote
24	30	73.2	237	2	C97948	hypothetical prote
25	30	73.2	392	2	H81408	probable periplasm
26	30	73.2	520	2	JS0291	intermediate filam
27	30	73.2	717	2	S78177	hypothetical prote
28	30	73.2	754	1	JC5314	CDC28/cdc2-like ki
29	30	73.2	770	2	S75042	hypothetical prote

30	30	73.2	859	1	S06418	3',5'-cyclic-GMP P
31	30	73.2	2244	2	F90563	hypothetical prote
32	30	73.2	3724	2	T18427	hypothetical prote
33	29	70.7	133	2	A41328	hypothetical prote
34	29	70.7	197	2	T38418	probable coiled-co
35	29	70.7	212	2	F97033	probable membrane-
36	29	70.7	231	2	A11262	ABC transporter, A
37	29	70.7	231	2	AC1625	ABC transporter, A
38	29	70.7	234	2	JT0874	purine-nucleoside
39	29	70.7	346	2	H72237	hypothetical prote
40	29	70.7	352	2	T51935	ribosomal protein
41	29	70.7	380	2	F81449	8-amino-7-oxononan
42	29	70.7	421	2	E69467	hypothetical prote
43	29	70.7	429	2	A10029	conserved hypothet
44	29	70.7	522	2	AD2344	hypothetical prote
45	29	70.7	524	2	S07168	probable maturase,

ALIGNMENTS

RESULT 1			
PH1050			
Ig light chain V region (clone 111-c1) - mouse (fragment)			
C/Species: Mus musculus (house mouse)			
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000			
C/Accession: PH1050			
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.			
J. Exp. Med. 176, 761-779, 1992			
A/Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c			
A/Reference number: PH0971; MUID:92381444; PMID:1512540			
A/Accession: PH1050			
A/Status: nucleic acid sequence not shown			
A/Molecule type: mRNA			
A/Residues: 1-103 <TIL>			
A/Experimental source: B cell, strain [NZB x NZW]F1			
C/Superfamily: immunoglobulin V region; immunoglobulin homology			
C/Keywords: immunoglobulin			
F;16-96/Domain: immunoglobulin homology <IMM>			
Query Match			
Best Local Similarity 100.0%; Score 41; DB 2; Length 103;			
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 KOSYNLRT 8		
Db	95 KOSYNLRT 102		
RESULT 2			
PH1101			
Ig light chain V region (clone 111.19) - mouse			
C/Species: Mus musculus (house mouse)			
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000			
C/Accession: PH1101			
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.			
J. Exp. Med. 176, 761-779, 1992			
A/Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c			
A/Reference number: PH0971; MUID:92381444; PMID:1512540			
A/Accession: PH1101			
A/Status: nucleic acid sequence not shown			
A/Molecule type: mRNA			
A/Residues: 1-104 <TIL>			
A/Experimental source: B cell, strain [NZB x NZW]F1			
C/Superfamily: immunoglobulin V region; immunoglobulin homology			
C/Keywords: immunoglobulin			
F;16-96/Domain: immunoglobulin homology <IMM>			
Query Match			
Best Local Similarity 100.0%; Score 41; DB 2; Length 104;			
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 KOSYNLRT 8		

Db 95 KQSYNLRT 102

## RESULT 3

PH1102

Ig light chain V region (clone 111.61) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1102

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1102

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-104 &lt;TIL&gt;

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 41; DB 2; Length 104;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

## RESULT 4

S41393

Ig kappa chain V region (12.5H VL) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001

C:Accession: S41393

R:Margaritte, C.; Brard, D.; Brard, F.; Tron, F.

submitted to the EMBL Data Library, January 1994

A:Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-DN

A:Reference number: S41393

A:Accession: S41393

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 &lt;MAR&gt;

A:Cross-references: EMBL:Z29536

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 41; DB 2; Length 112;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

## RESULT 5

S43103

Ig kappa chain V-J region (4B1 VL) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-May-2001

C:Accession: S43103

R:Gilbert, D.; Brard, F.; Margaritte, C.; Delpech, A.; Tron, F.

submitted to the EMBL Data Library, March 1994

A:Description: An idiotype D23-bearing polyclonal, murine anti-DNA monoclonal antibody

A:Reference number: S42484

A:Accession: S43103

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 &lt;GIL&gt;

A:Cross-references: EMBL:Z31353; NID:G467574; PIDN:CAA83231.1; PID:G467575

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 41; DB 2; Length 112;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

## RESULT 6

PS0023

Ig kappa chain precursor V region (6A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000

C:Accession: PS0023

R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.

Gene 74, 335-345, 1988

A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of e

A:Reference number: PS0023; MUID:89232725; PMID:3149944

A:Accession: PS0023

A:Molecule type: mRNA

A:Residues: 1-133 &lt;MAR&gt;

A:Experimental source: strain BALB/c

A:Note: the amino-terminal four residues of the mature protein were directly sequenced

C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aerugin

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

F:21-133/Product: Ig kappa chain V region 6A4 #status experimental &lt;IGV&gt;

F:36-116/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 41; DB 2; Length 133;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 115 KQSYNLRT 122

## RESULT 7

A42575

Ig kappa chain V region (anti-angiotensin II) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: A42575

R:Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.

Science 257, 528-531, 1992

A:Title: Recognition of angiotensin II: antibodies at different levels of an idiotypic ne

A:Reference number: A42575; MUID:92342952; PMID:1636087

A:Accession: A42575

A:Molecule type: mRNA

A:Residues: 1-97 &lt;GAR&gt;

A:Cross-references: GB:S40673; NID:G252096; PIDN:AAB22668.1; PID:G252097

A:Experimental source: BALB/c mice, myeloma cell line NS-1

A:Note: sequence extracted from NCBI backbone (NCBIN:109331, NCBIP:109336)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-88/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 97;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 87 KQSYNLRT 94

RESULT 8

PH1047

Ig light chain V region (clones 165.45 and 163-cl) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1047, PH1049

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1047

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-103 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 103;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

RESULT 9

PH1051

Ig light chain V region (clone 165.3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1051

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1051

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-103 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 103;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

RESULT 10

PH1052

Ig light chain V region (clone 165.5) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1052

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1052

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-103 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 103;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

RESULT 11

PH1103

Ig light chain V region (clone 111.109) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1103

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1103

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-104 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 104;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

RESULT 12

PT0408

Ig light chain V region (S107/VH11 group 1-6) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PT0408

R/Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A/Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A/Reference number: PT0376; MUID:91147903; PMID:1900082

A/Accession: PT0408

A/Molecule type: DNA

A/Residues: 1-113 <BEH>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 113;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8

Db 95 KQSYNLRT 102

RESULT 13

PT0407

Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PT0407



R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
J. Exp. Med. 173, 731-741, 1991  
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody  
A;Reference number: F10376; MUID:91147903; PMID:1900082  
A;Accession: F10407  
A;Molecule type: DNA  
A;Residues: 1-113 <BEH>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 34; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 3.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
|||:|:  
Db 95 KQSYNLRT 102

RESULT 14

F97819  
hypothetical protein RC0958 [imported] - Rickettsia conorii (strain Malish 7)  
C;Species: Rickettsia conorii  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: F97819  
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R  
Science 293, 2093-2098, 2001  
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A;Reference number: A97700; MUID:21442074; PMID:11557893  
A;Accession: F97819  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-50 <KUR>  
A;Cross-references: UNIPROT:Q92H14; GB:AE006914; PIDN:AAL03496.1; PID:G15620070; GSPDB:C  
C;Genetics:  
A;Gene: RC0958

Query Match 78.0%; Score 32; DB 2; Length 50;  
Best Local Similarity 85.7%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 7  
|||:|:  
Db 37 KQSYNLQ 43

RESULT 15

S53840  
hypothetical protein 83 - Acanthamoeba castellanii mitochondrion  
C;Species: mitochondrion Acanthamoeba castellanii  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S53840  
R;Burger, G.; Plante, I.; Loneragan, K.M.; Gray, M.W.  
J. Mol. Biol. 245, 522-537, 1995  
A;Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: comp  
A;Reference number: S53825; MUID:95147275; PMID:7844823  
A;Accession: S53840  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-83 <BUR>  
A;Cross-references: UNIPROT:Q33664; GB:U12386; NID:G562028; PIDN:AAD11832.1; PID:G562044  
A;Experimental source: strain Neff; ATCC 30010  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C;Genetics:  
A;Genome: mitochondrion  
A;Genetic code: SGC6  
C;Keywords: mitochondrion

Query Match 78.0%; Score 32; DB 2; Length 83;  
Best Local Similarity 62.5%; Pred. No. 6.1;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLRT 8  
|||:|:  
Db 12 KQSFNIKT 19

Search completed: March 1, 2005, 17:44:47  
Job time : 11.8308 secs



Q9GHC8  
ID Q9GHC8 PRELIMINARY; PRT; 515 AA.  
AC Q9GHC8;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis umbellata.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=120002;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040195; BAB16803.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61977 MW; BA896191DB66FD6F CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLR 7  
|||  
234 KQSYNLR 240

RESULT 3  
Q9GHC9  
ID Q9GHC9 PRELIMINARY; PRT; 515 AA.  
AC Q9GHC9;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040194; BAB16802.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61852 MW; 2B33690D42B60290 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;

Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KQSYNLR 7  
|||  
234 KQSYNLR 240

RESULT 4  
Q9GHD0  
ID Q9GHD0 PRELIMINARY; PRT; 515 AA.  
AC Q9GHD0;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040193; BAB16801.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61844 MW; 1BBFF413F5DE7848 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLR 7  
|||  
234 KQSYNLR 240

RESULT 5  
Q9GHD1  
ID Q9GHD1 PRELIMINARY; PRT; 515 AA.  
AC Q9GHD1;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040192; BAB16800.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.

DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturse2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturas2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61747 MW; 66A8A11DDA39BFBB CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

RESULT 6

O9GHD2 PRELIMINARY; PRT; 515 AA.

AC Q9GHD2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matK;  
OS Helionopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matK gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040191; BAB16799.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturse2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturas2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61780 MW; A4932FD7A8600BA8 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

RESULT 7

O9GHD3 PRELIMINARY; PRT; 515 AA.

AC Q9GHD3;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matK;  
OS Helionopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matK gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040190; BAB16798.2; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturse2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturas2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61923 MW; 898AAB45F7477E9F CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

RESULT 8

O9GHD4 PRELIMINARY; PRT; 515 AA.

AC Q9GHD4;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matK;  
OS Helionopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matK gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040189; BAB16797.2; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturse2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_maturas2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61834 MW; 590865E229969D6 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

RESULT 9

O9GHD5 PRELIMINARY; PRT; 515 AA.

AC Q9GHD5;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)



DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis orientalis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040188; BAB16796.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61856 MW; 11FC132987377A59 CRC64;

Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

RESULT 10  
Q9GHD6 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD6;  
AC Q9GHD6;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis leucantha.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=120001;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040187; BAB16795.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61977 MW; BA896191DB66FD6F CRC64;

Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

Db 234 KQSYNLR 240

RESULT 11  
Q9GHD7 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD7;  
AC Q9GHD7;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Heloniopsis kawaiol.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Heloniopsis.  
OX NCBI\_TaxID=120000;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040186; BAB16794.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61859 MW; 6480F5F43AA86738 CRC64;

Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

RESULT 12  
Q9GHD8 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD8;  
AC Q9GHD8;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Ypsilandra tibetica.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Ypsilandra.  
OX NCBI\_TaxID=120020;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040185; BAB16793.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.



KW Chloroplast.  
SQ SEQUENCE 515 AA; 61796 MW; 1C8FF71CAF6CEFF8 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 234 KQSYNLR 240

## RESULT 13

O7YJL7

PRELIMINARY; PRT; 521 AA.

ID O7YJL7  
AC O7YJL7;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matK;  
OS Chortolirion angolense.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asphodelaceae;  
OC Chortolirion.  
OX NCBI\_TaxID=210957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Treutlein J., Smith G.F., van Wyk B.-E., Wink M.;  
RT "Phylogenetic relationships in Asphodelaceae (subfamily Allooideae)  
inferred from chloroplast DNA sequences (rbcl, matK) and from genomic  
fingerprinting (ISSR).";  
RL Taxon 52:193-207(2003).  
DR EMBL: AJ511393; CAD54537.1; -;  
DR GO: GO:0008380; P:RNA splicing; IEA.  
DR InterPro: IPR008998; Agglutinin.  
DR InterPro: IPR000442; Intron maturase2.  
DR InterPro: IPR002866; MatK\_N.  
DR Pfam: PF01348; Intron\_maturase2; 1.  
DR Pfam: PF01824; MatK\_N; 1.  
SQ SEQUENCE 521 AA; 62846 MW; 8841EAA964DA0343 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 521;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 235 KQSYNLR 241

## RESULT 14

O7YJL7

PRELIMINARY; PRT; 521 AA.

ID O7YJL7  
AC O7YJL7;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matK;  
OS Aloe ramosissima.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asphodelaceae;  
OC Aloe.  
OX NCBI\_TaxID=210944;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Treutlein J., Smith G.F., van Wyk B.-E., Wink M.;  
RT "Phylogenetic relationships in Asphodelaceae (subfamily Allooideae)  
inferred from chloroplast DNA sequences (rbcl, matK) and from genomic  
fingerprinting (ISSR).";

RL Taxon 52:193-207(2003).

DR EMBL: AJ511370; CAD54514.1; -;  
DR GO: GO:0008380; P:RNA splicing; IEA.  
DR InterPro: IPR008998; Agglutinin.  
DR InterPro: IPR000442; Intron\_maturase2.  
DR InterPro: IPR002866; MatK\_N.  
DR Pfam: PF01348; Intron\_maturase2; 1.  
DR Pfam: PF01824; MatK\_N; 1.  
SQ SEQUENCE 521 AA; 62784 MW; 58B661FF1185922E CRC64;

Query Match 87.8%; Score 36; DB 2; Length 521;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 7  
|||  
Db 235 KQSYNLR 241

## RESULT 15

O6NSV1

PRELIMINARY; PRT; 186 AA.

ID O6NSV1  
AC O6NSV1;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Possible flavin-dependent oxidoreductase.  
GN OrderedLocustNames=RP2869;  
OS Rhodopseudomonas palustris.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Rhodopseudomonas.  
OX NCBI\_TaxID=1076;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CGA009 / ATCC BAA-98;  
RX PubMed=14704707; DOI=10.1038/nbt923;  
RA Larimer F.W., Chain F., Hauser L., Lamerdin J.E., Malfatti S., Do L.,  
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,  
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,  
RA Harrison F.H., Gibson J., Harwood C.S.;  
RT "Complete genome sequence of the metabolically versatile  
photosynthetic bacterium Rhodopseudomonas palustris.";  
RL Nat. Biotechnol. 22:55-61(2004).  
DR EMBL: BX572602; CAE28310.1; -;  
DR InterPro: IPR005025; FMN\_red.  
DR Pfam: PF03358; FMN\_red; 1.  
KW Complete proteome.  
SQ SEQUENCE 186 AA; 20152 MW; E7D868C8DD44064E CRC64;

Query Match 80.5%; Score 33; DB 2; Length 186;  
Best Local Similarity 75.0%; Pred. No. 42;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KQSYNLR 8  
||:|:|  
Db 16 KQAYSLRT 23

Search completed: March 1, 2005, 17:43:20  
Job time : 52.8154 secs

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